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               Copyright
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rvat	OBSEQUENCE 20, APPLICATION US/OBB atent No. 6127116 GENERAL INFORMATION: APPLICANT: Rice, Charles e TITLE OF INVENTION: FUNCTIO TITLE OF INVENTION: PUNCTIO TITLE OF INVENTION: PUNCTIO TITLE OF INVENTION: VIRUS ( TORRESPONDENCE ADDRESS: 21 CORRESPONDENCE ADDRESS: 21 CORRESPONDENCE ADDRESS: 21 COUNTRY: USA STREET: Floor CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601 CMEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DOS/ SOFTWARE: PatentIn Releas CURRENT APPLICATION NUMBER: US/OB FILING DATE: 03-MAR-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David REGISTRATION NUMBER: 26,7. REFERENCE/DOCKET NUMBER: 75000 TELEPHONE: 201-43-1604 REGISTRATION FOR SEQ ID NO: 20 SEQUENCE CHARACTERISTICS: LENGTH: 3011 amino acids TYPE: amino acids STRANDEDNESS: single MOLECULE TYPE: protein HYPOTHETICAL: NO PRAGMENT TYPE: N-terminal 08-B11-566-20	22223334444444444444444444444444444444
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                                                 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: FUNCTIONAL DNA CLONE TITLE OF INVENTION: VIRUS (HCV) AND USES NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1050
                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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                                 SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 111
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Ave, Continental Plaza, STREET: Floor
                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 03-MAR-1997
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                                                                                                                                                                                                                               US/08/811,566
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; HYPOTHETICAL:
; FRAGMENT TYPE:
US-08-811-566-2
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US-08-221-750A-5
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                                                                                                                                                                                                                                                                             Sequence 5, Application US/08221750A Patent No. 5643747
GENERAL INFORMATION:
APPLICANT: Baker, Steven M.
APPLICANT: Deich, Robert A.
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Best Local Similarity
Matches 100; Conserv
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC -DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/221,750A
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                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                   ZIP:
                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                Smith & Reynolds,
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RESULT 4
US-08-444-818-66
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                                                                                                                                                                                                                              Sequence 66, Application US/08444818 Patent No. 6150087 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                               ADDRESSEE: Chiron Corporation
                                                                                                                                                                 APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NAMBU Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
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REFERENCE/DOCKET NUMBER: ACC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      363
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                                                                  COUNTRY:
                                                                                                      CITY:
                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                  POAFWLMASLAGLA 416
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25.7%; Pred. No. 0.(
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Best Local Similarity 20.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
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LENGTH: 2261 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                          425
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                                                                                   446 SFW-OPOPSKOLPP
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                     AACGDIINGLPVSARRGREILLGPADGMVSKGWRLL-APITAYAQQTRGLLGCIITSLTG 424
                                                                                                                                                                                                                                                                                            RDRN------PQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTL-WWLCIGAIA 445
                                                                                                                                                                                                                                AVEGGLL ----
                                                                                                                                                                                                                                                            VQMVIIK--LGALTGTYVYNHLTPLRDWAH-NGLRDLAVAVEPVVFSQMETKLITWGADT 365
                                                                                                                                                                                                                                                                                                                                 PTLVFDITKLLLAVFGPLWILQASLLKVPYFVRVQGLLRFCALARKMIGGHY----- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADFTSRVYSYLGN-PNLLAAYLVPTTAFS-----AAAIGVWRGWLPKLLAIAATGASSLC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLVSFLVFFCFA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRNSV 182
                                                                                                                    RDKNQVEGEVQIVSTAAQTF-LATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDL 483
                                                                                                                                                                                                                                                                                                                                                                  LSPYYKR-----YISWCLWWLQYFLTRVEAQLHVWIPPLNVRGGRDAVILLMCAVH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------VYTEYGMWPLLLLLLALPQRAYALDTEVAASCG------GVVLVGLMALT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                   458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.7%; Score 114.5; DB
20.6%; Pred. No. 0.029;
ative 55; Mismatches 1
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                                                                                                                                                                                                                         ----GLTAFAWLLLVTAVTAVRQVSR-----LR 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----WYLKGKWVPGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- 161
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23;

US-08-444-818-75
, Sequence 75, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-444-818-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/08/403,590
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 0310.002
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEPHONE: (508)359-3876
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 2436 amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 102; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NAMBY Diagnostics and Vaccines NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 GLVSFLVFFCFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 KLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRNSV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 VGSSIASWAIKWEYVVLLFLLLADARVCSCL-WMMLLISQAEAALENLVILNAASLAGTH 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LGLGLAAIAAYW---ALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVGLA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/444,818 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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RDKNQVEGEVQIVSTAAQTF-LATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDL 658
                                                RDRN------
                                                                                            AACGDIINGLPVSARRGREILLGPADGMVSKGWRLL-APITAYAQQTRGLLGCIITSLTG 599
                                                                                                                                          VQMVIIK--LGALTGTYVYNHLTPLRDWAH-NGLRDLAVAVEPVVFSQMETKLITWGADT 540
                                                                                                                                                                                                                               LSPYYKR-----YISWCLWWLQYFUTRVEAQLHVWIPPLNVRGGRDAVILLMCAVH 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADETSRYYSYLGN-PNLLAAYLVPTTAFS-----AAAIGVWRGWLPKLLAIAATGASSLC 236
                                                                                                                                                                                                                                                                                  PTLVFDITKLLLAVFGPLWILQASLLKVPYFVRVQGLLRFCALARKMIGGHY-----
                                                                                                                                                                                                                                                                                                                              ------LLVAVLG-----LEPLRVRVLSIF----VGREDSSNNFRINVWLAV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VYTFYGMWPLLLLLLALPQRAYALDTEVAASCG------GVVLVGLMALT 380
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                                              --PQAFWLMASLAGLAGMLGHGLEDTVLYRPEASTL-WWLCIGAIA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----WYLKGKWVPGA----- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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237 LILTYSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPV-VLGGLVAV 287	γQ	
673GVTTEYGMWPLLLLLLALPQRAYALDTEVAASCG	₽b	
183 ADETSRVYSYLGN-PULLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLC 236	Qγ	
650 GLVSFLVFFCFA 672	Db	
123 KLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRNSV 182	Qy	
591 VGSSIASWAIKWEYVVLLFLLLADARVCSCL-WMMLLISQAEAALENLVILNAASLAGTH 649	DЬ	
	Qy	
ery Match 4.7%; Score 114.5; DB 4; Length 2772; st Local Similarity 20.6%; Pred. No. 0.04; tches 102; Conservative 55; Mismatches 160; Indels 177; Gaps	Query Best   Match	
MOLECULE TYPE -444-818-89	; 0s-08	
ogy: li	٠. ٠	
TELEFAX: (508)359-3885		
TELEPHONE: (508)359-3876		
ч		
NUMBER: 33,		
EY/AGENT		
DATE:		
DATA:	•••	
CLASSIFICATION: 424	<b></b>	
APPLICATION NUMBER: US/08/444,818		
ease #1.0/ version #1.		
OPERATING SYSTEM: PC-DOS/MS-DOS		
COMPUTER: IBM PC compatible	•• •	
READABL		
ZIP: 94608-2916		
COUNTRY: USA		
CITY: Emeryville	٠.	
4560 Horton Street	٠. ٠	
ATDRESSEE: Chiron Corporation		
NUMBER OF SEQUENCES: 777		
APPLICANT: Chien, David Y. APPLICANT: Rutter, William J.		
NFORMATION:		
Sequence 89, Application US/U8444818 Patent No. 6150087		
8-89	ശല	
659 VGWPAPQGSRSLTP 672	Db	
440 SEW-CPCP-SACEPF 430	Qy	

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US-08-466-975A-23
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/9:
APPLICATION NUMBER: US 07/9:
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT.
TITTING DATE: 13-DEC-1991
                                                                                                                        TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino aci
HYPOTHETICAL: N
ANTI-SENSE: NO
8-466-975A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
                                 MOLECULE TYPE: pe
                                                                                                                                                                                                REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9:
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DELEYS, ROBERT J
APPLICANT: POLLET, DIRK
APPLICANT: WAERTENS, GEERT
APPLICANT: VAN HEUVERSWUN, HUGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 VQMVIIK--LGALTGTYVYNHLTPLRDWAH-NGLRDLAVAVEPVVFSQMETKLITWGADT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 SFW-QPQPSKQLPP 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       936 RDKNQVEGEVQIVSTAAQTE-LATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDL 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               877 AACGDIINGLPVSARRGREILLGPADGMVSKGWRLL-APITAYAQQTRGLLGCIITSLTG 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  995 VGWPAPQGSRSLTP 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AVEGGLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ARLINGTON
STATE: VA
                                                                    TOPOLOGY:
                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDRN-----PQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTL-WWLCIGAIA 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08466975A
                                                                                                                          2894 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                      linear
                                                peptide
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                                                                                                                                                                                                                                                                                                                             EP 90124241.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23, Application US/08391671A Patent No. 5922532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DELEYS, R
APPLICANT: POLLET, D
APPLICANT: MAERTENS,
APPLICANT: VAN HEUVE
                                                                                          COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MAERTERS, GEERT
APPLICANT: VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION
TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1109 VGWPAPQGSRSLTP 1122
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1050
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                                    FILING DATE: 21-FEB CLASSIFICATION: 435
                                                                                                                                                                                                                                                                    STREET: 1100 NO CITY: ARLINGTON
                                                                                                                                                                                                            COUNTRY: UZIP: 22201
                                                                                                                                                                                                                                                   STATE:
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                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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1100 NORTH GLEBE ROAD
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                                                     21-FEB-1995
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                                                                           US/08/391,671A
  US 07/920,286
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                                                                                                                Version #1.30
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             Sequence 23, Application US/08467902A Patent No. 6007982 GENERAL INFORMATION:
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Best Local Similarity
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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LENGTH: 2894 amino aci
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                            1109 VGWPAPQGSRSLTP 1122
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APPLICANT:
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                                                                                                                                                                                                                                                                                        368 AVEGGLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,663
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STRANDEDNESS: si
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                                                                                                                                                                                                                       RDRN-------PQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTL-WWLCIGAIA 445
                                                                                                                                                                                                                                                        AACGDIINGLPVSARRGREILLGPADGMVSKGWRLL-APITAYAQQTRGLLGCIITSLTG
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DELEYS, ROBERT J
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13-DEC-1991
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14-DEC-1990
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Pred. No. 0.042;
55; Mismatches 1
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; HYPOTHETICAL:
; ANTI-SENSE: 1
US-08-467-902A-23
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: 1
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APPLICANT: VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                    705 VGSSIASWAIKWEYVVLLELLLADARVCSCL-WMMLLISQAEAALENLVILNAASLAGTH 763
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TO38164100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/920,286 FILING DATE: 14-OCT-1992
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                                    LSPYYKR-----YISWCLWWLQYFLTRVEAQLHVWIPPLNVRGGRDAVILLMCAVH 881
                                                                                                                ADFTSRVYSYLGN-PNLLAAYLVPTTAFS----AAAIGVWRGWLPKLLAIAATGASSLC
                                                                       LILTYSRGGWLGEVAMIFVWALLGLYWFQPRLPAPWRRWLEPV-VLGGLVAV-----
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1100 NORTH GLEBE ROAD
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20.6%; Pred. No. 0.0
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5; Mismatches 1
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--LEPLRVRVLSIF----VGREDSSNNFRINVWLAV 324
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                                                                                                                                                                                                 TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-FEB-1995
APPLICATION NUMBER: US 07/
FILING DATE: 14-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino aci
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APPLICANT: POLLET, DIRK
APPLICANT: MAERTENS, GEERT
APPLICANT: WAN HEUVERGMUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION
TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIRUS
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APPLICATION NUMBER:
FILING DATE: 14-DEC-
       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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No. 6287761
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14-DEC-1990
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; ANTI-SENSE:
US-09-275-265-23
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Best Local Similarity
Matches 102; Conserv
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      APPLICANT: Chien, David Y,
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NAMBY Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
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                                                      FILING DATE:
                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                    CITY: Emeryville
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20.68;
 US/08/403,590
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Pred. No. 0.042;
55; Mismatches 160;
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FILING DATE: 14-MAR-1995 ATTORNEY/AGENT INFORMATION: NAME: Harbin, Alisa A.

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RESULT 12
US-08-440-103-36
US-08-440-103-36
; Sequence 36, Application US/08440103
; Patent No. 5670152
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                                                                                      GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2995 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
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TOPOLOGY:
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                                   CITY:
                                                       STREET:
COUNTRY:
                   STATE:
                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                        VGWPAPQGSRSLTP 1122
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                                                                                                                                Polypeptide Compositions
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Best Local :
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TELEFAX: (510) VI
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
FRIGTH: 3011 amino acids
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FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,103
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 4.7%; Score 114.5; DB 1;
Local Similarity 20.6%; Pred. No. 0.045;
hes 102; Conservative 55; Mismatches 160;
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VGWPAPQGSRSLTP 1122
                                   SFW-QPQPSKQLPP
                                                                         RDKNQVEGEVQIVSTAAQTF-LATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDL 1108
                                                                                                                                                     AACGDIINGLPVSARRGREILLGPADGMVSKGWRLL-APITAYAQQTRGLLGCIITSLTG
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Best Local Similarity 20.6
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BArbara G.
REGISTRATION NUMBER: 33.113
REFERENCE/DOCKET NUMBER: 021
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
NUMBER OF SEQUENCES: 45
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CORRESPONDENCE ADDRESS:
                                                                                                                    831
                                              882 PTLVFDITKLLLAVFGPLWILQASLLKVPYFVRVQGLLRFCALARKMIGGHY------
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/440,542 FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                            LGLGLAAIAAYW---ALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVGLA 122
                                                                                                               LSPYYKR-----YISWCLWWLQYFLTRVEAQLHVWIPPLNVRGGRDAVILLMCAVH 881
                                                                                                                                                                              ------VYTFYGMWPLLLLLLALPQRAYALDTEVAASCG------GVVLVGLMALT 830
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Pred. No. 0.045;
5; Mismatches 160;
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Patent No.
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Best Local
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COUNTRY: U.S...
ZIP: 94662-8097
ZIP: PORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
PC-DOS/MS-DOS
COMPAND TO THE PC-DOS/MS-DOS
COMPAND TO THE PC-DOS/MS-DOS
COMPAND TO THE PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
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NAME: Blackburn Esq., Rober
REGISTRATION NUMBER: 30,447
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (51) 601-2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
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FILING DATE: 07-JUL-1992
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-----VYTFYGMWPLLLLLLALPQRAYALDTEVAASCG------GVVLVGLMALT 830
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                                                                                                    KLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNOWIYGVEELATWVDRNSV 182
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Pred. No. 0.045;
5; Mismatches 1
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Best Local Similarity

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; MOLECULE TYPE: US-08-440-519-10
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US-08-440-519-10
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                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
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                                                                                                             TELEFAX: (510) 655-35 INFORMATION FOR SEQ ID NO:
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APPLICANT: Choo, George
APPLICANT: Kno, George
TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/910,760 FILING DATE: 07-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 601-2702
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                                                                                                                                                                                                  NAME: Blackburn Esq., Rober REGISTRATION NUMBER: 30,447
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Emeryville
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                                     TOPOLOGY:
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Query Match

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                                                             RDKNQVEGEVQIVSTAAQTF-LATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDL 1108
                                                                                          RDRN--------PQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTL-WWLCIGAIA
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Search completed: January 10, Job time: 2317 sec 2002, 23:04:50

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Result
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Maximum DB seq length: 200000000
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Perfect score:
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1: /SIDS2/gcgdat
2: /SIDS2/gcgdat
                                                                                                                                                                                                                                                                                                                                                                            | SIDS2/gcgdata/geneseq/geneseqp/AA198.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp/AA199.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT: *
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Copyright (c) 1993 - 2000 Comp
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                                                          11245590
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                              Bacterial general
Streptococcus pneu
Corynebacterium gl
C glutamicum prote
Virulence gene pro
Pseudomonas aerugi
C glutamicum prote
C. glutamicum SRT
Neisseria meningit
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 Neisseria
                    Neisseria
meningit
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4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7			4.8	.80	80			.9		.9	.9	.9			
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a	Hepatitis C virus	Hepatitis C virus	HCV polyprotein.	HCV polyprotein.	C	Hepatitis C virus	Compiled HCV seque	Polyprotein encode	ш	hepatit	Composite HCV HC-J	ncoded b	Hepatitis C virus	ñ	Peptide encoded by		HCV pòlypeptide 1.	Sequence encoded i	Peptide encoded by	NANBH virus strain		Bordetella pertuss	Rat L-type amino a	₹	Hepatitis C virus-	Hepatitis C virus	Mycobacterium tube	Human L-type amino	Human membrane tra	Human ORFX ORF2900	C glutamicum prote	ria meningi	Murine edg6 protei	

## ALIGNMENTS

RESULT AAY22569 ID AAY2

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AAY22569 standard; Protein;

388

A

17-NOV-1999 (first entry)

AAY22569;

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WPI; 199
N-PSDB;
             Streptococcus pneumoniae general essential protein genes and proteins, useful for identification of antibacterial agents - \!\!\!
                                                                 Youngman P,
                                                                                                 31-DEC-1997;
                                                                                                                  30-DEC-1998;
                                                                                                                                   08-JUL-1999.
                                                                                                                                                                    Streptococcus
                                                                                                                                                                                    General essential protein; pathogenic bacteria; pathogen; inhibitor; bacterial growth.
                                                                                                                                                                                                             Bacterial general
                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                    W09933871-A2.
                                       1999-430230/36.
DB; AAZ20360.
                                                               Fritz C,
                                                                                                                                                                    pneumoniae.
                                                                                                 97US-0070116
                                                                                                                  98WO-US27918.
                                                                                                                                                                                                             essential protein gep1713
                                                               Murphy
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                                                                Guzman
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Claim 1; Fig 13; 124pp; English.

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AAY81570
AAY81570
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     addition, the operons containing genes encoding GEP and the polypeptides themselves, are useful targets for identifying compounds that are inhibitors of the pathogens in which the GEP are expressed. Such inhibitors are useful for inhibiting bacterial growth by being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a Streptococcus pneumoniae general essential protein (GEP) protein of the invention. The genes encoding the GEP polypeptides are useful molecular tools for identifying similar genes pathogenic microorganisms, such as pathogenic strains of Bacillus. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                   27-JUL-1999;
                                                                                                                    Streptococcus
                                                                                                                                                   pneumococcal disease
                                                                                                                                                                  Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagno
                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                    24-MAY-2000
                                                                                                                                                                                                                                                                                       AAY81520;
                                                                                                                                                                                                                                                                                                                    AAY81520 standard;
                                                    10-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                    gkrpi-iglylsfltvvavhgifdlalf----
                                                                                                                                                                                                                                                                                                                                                                                                                                   NPQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTLWWLCIGAI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVYPLYQQARFTA---LSAYSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDR 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fieklkg-----lsskeli----llgiilsi-----flp---fylfvvvlclyiisli 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----gfv-----nlfglnftq-----nrtafpaiiagaiiylfttiknwkaf 233
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                                                                                                                                                                                                                                                      (first entry)
                                                                                                                  pneumoniae
                                                                                                                                                                                                                     pneumoniae type 4 protein sequence #20
                    99WO-GB02451.
                                                                                                                                                                                                                                                                                                                      Protein;
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Pred. No. 1.6e-06;
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AAB79584
ID AAB
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AAB79584 standard;

Protein;

30-APR-2001 AAB79584;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and/or antigens. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 74; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents
                                                                                                                                                                                                                                                                                                  120
 308
                                                                                                                                                  199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 HWLVLLYWGVDALATGLSP--VRAAALVGLAKLTLYLLVFALAARVLRNPRLRSLLFSVV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibiting expression of the protein
vavhgifdlalf-----
                                     MLGHGLFDTVLYRPEASTLWWLCIGAI 444
                                                                                                           LSAYSVPLEVAVEGGLLGLTAFAWLLLYTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAG
                                                                                                                                                                                   VRVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGN--TAFNLVYPLYQQARFTA
                                                                                                                                                                                                                    ---nlfglnftq-----nrtafpailagailylfttiknwkafwlsigvfaiglsflf 198
                                                                                                                                                                                                                                                             FVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAV-----
                                                                                                                                                                                                                                                                                                  cfcimiafylftttkln-----wlkvfcvia------gfv---
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                                                                                                                                                                                                                                                                                                                                                                                                                                              hpmlllflsystvisilaqnwmglvasvgmflftifflhy---qsilshkffrliiqfvl 67
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                                                                                                                                                                                                                                                                                                                                     ----LLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILTYSRGGWLGFVAMI 253
                                                                                                                                                                                                                                                                                                                                                                        fgsvlsaafaslehfqivkkfnyaflspnmqvwhqnraevtff-----
                                                                        -hahslyidtilsygivgti----llvlssvapvrlmmdmsqesgkrpi-iglylsfltv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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99US-0125164.
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20.2%;
 wiqsgfi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 143.5; DB 2
Pred. No. 2.5e-06;
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08-JUL-1999

08-JUL-1999
                                 metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a dial, a carbohydrate, an aromatic compound, a vitamin, a composition of the compound of the compound of the compound of the composition of the compound of the compou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                      carbohydrates
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                polyketide,
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18-DEC-2000;
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                                                                                   Corynebacterium
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                                                                                                                          bacterium;
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2000EP-0127688
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSFLHR-----LFGSLRAWRASSQLLVWSEALGGFLLAVVYGSAPFVPSSALGLGLAA 72
                                                                                                                                                                                                                                                                                      RVYSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILTYSRGGWL
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                                                                                                                                                                                                                                                                                                                                 mligvidhqt-gtrdirrlgflvkkmpftfvsv----ligalsmas
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                                                                 atgndilsmlvyranllgkffgrmadsmsprrhlvslivllwalaafatihpsvqlapkq
                                                                                                GPGNTAFN-LVYPLYQQARFTALSAYSVPLE---VAVEGGLLGLTAFA-----
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                                                                                                                                                                                                   -----vlgafvdgprdmshvkeapvslwl-paalpglmslplvlvlslfdapvsa
                                                                                                                                                                                                                                  GEVAMIEVWALLGLYWEQPR-----LPAPWRRWLEPVVLGGLVAVLLVAVLGLEPLRVRV
                                                                                                                                                                                                                                                                 pllgfvskegmi-----tafmdapig--nsyvvlllvgaaiga-----vltftysakl
pgidrwidliplaiialsvfgllttrn---
                                                                                                                                aatsaageaahmhlalwhgintpllislgvlvagilgvlfrkelw----kiaetspf-pi
                                -----WILLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLGHGL-FDTVLY-RPEA 433
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2000JP-0159162.
2000JP-0280988.
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Pred. No. 0.00014;
7; Mismatches 188
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Ozaki A;
---rlsaavlvgtvgvgvsfqmlllgapdv
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Best Local (
                                                                                                                                                                                                                                                                                              The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence ge from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may i mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis a
                                                                                                                                                                                                                                                                                                                                                                                                                             genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virulence gene; septicemia; bror
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virulence gene protein
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                                                                                                                                                                                                                                                                                     wound infections.
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DB; AAC79616.
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-illahl ffnvplacrlflqglqaipvqqrqlaaqlnlrgwhfirliewpylrqqllpaf\\
                            NLLAAYL---
                                                                         RNPRLRSLLFSVVVITSLF---VSVYGLNOWIYGVEELATWVDRNSVADFTSRVYSYLGNP
                                                                                                 al-lsdqylq----hviifsfw----qaflsavlavlfggivaraffyqpfvgkklil
                                                                                                                        LLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVGLAKLTLYLLVFALAARVL 138
                                                ---klfsltfvlpalvaifgllgvygasgwlamlsqffaw--
                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                   useful as a live attenuated vaccine against bacterial infections
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                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                              536 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bronchopneumonia;
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99US-0153453
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                                                                                                                                                                                                  Score 130; DB
Pred. No. 0.00
47; Mismatches
                         -VPTTAFSAAAIGVWRGW---
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rhinitis;
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. 0.00011;
ches 139;
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                            ----LPKL
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 the pili, resulting in antigenic glycosylated pili useful as a vaccine against infection with that strain. A claimed multivalent vaccine against foremengative bacterial (GhB) infections comprises a group of pilin-glycan conjugates of different GhB strains or species. Methods for diagnosing GhB infection, P. aeruginosa diagnosis, treatment or amelioration of GhB infection, producing glycosylated pilin, testing agents capable of inhibiting adhesion of GhB pili to cells, preventing GhB infection or symptoms, and
                                                                                                                                                  This sequence comprises the pilO polypeptide of Pseudomonas aeruginosa group 1 strain 1244. It was deduced from an isolated DNA fragment (see AAT72332) identified downstream of the pilin
                                                                                                          structural gene (pilA). The pilO gene product glycosylates the pilO of P. aeruginosa strains by adding the specific O antigen components of the lipopolysaccharide carried by that strain onto
                                                                                                                                                                                                             Claim 4; Page 40-42; 60pp; English.
                                                                                                                                                                                                                                                                                                                                           Castric P,
                                                                                                                                                                                                                                            Gram-negative bacterial infections
                                                                                                                                                                                                                                                       DNA encoding Pseudomonas aeruginosa pilo useful to develop products to diagnose and
                                                                                                                                                                                                                                                                                                 WPI; 1997-351043/32.
N-PSDB; AAT72332.
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22-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PilO; pilin; glycosylation; Gram-negative bacterium;
                                                                                                                                                                                                                                                                                                                                                                      (USSA ) USARMRMC US ARMY MEDICAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                          Cross A,
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95US-0009190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
preventing GnB infection or symptoms,
                                                                                                                                                                                                                                                                                                                                           Sadoff J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain 1244.
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                                                                                                                                                                                                                                                                                                                                                                      MATERIAL
                                                                                                                                                                                                                                                       which glycosylates pilin, in vaccines for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection;
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Best Local
                                                                                                                               16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                        Nakagawa
Tateishi
Novel polynucleotides derived from Coryneform bacteria, fundation point of a gene, measuring expression of a gene,
                                                                                                                                                                                                                                                                         organic acid synthesis.
                                                                                                                                                                                                                                                                                                           C glutamicum protein fragment SEQ ID NO: 3588
                                       N-PSDB;
                                                                                                                                                                                                      20-JUN-2001
                                                                                                                                                                                                                            EP1108790-A2
                                                                                                                                                                                                                                                   Corynebacterium
                                                                                                                                                                                                                                                                                    Coryneform bacterium;
                                                                                                                                                                                                                                                                                                                                    26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                 AAG89834 standard; Protein;
                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                              18-DEC-2000;
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2000JP-0280988.
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Best Local S
Matches 97
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
Corynebacterium glutamicum; stress; resistance; tolerance; SRT; fine chemical production; organic acid; proteinogenic amino acid; proteinogenic amino acid; purine base; pyrimidine base; nucleonucleotide; lipid; saturated fatty acid; unsaturated fatty acid;
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                                                                                       SRT protein sequence SEQ
                                                                                                                                                                                             Protein;
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22.9%; Pred. No. 0.00036;
tive 50; Mismatches 129
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fatty acid; diol;
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117 ALVGLAKLTLYLLVFALAARVLRNPRLRSLLFS-----VVVITSLFVSVYGLNQWIYGV 170 | | | :|| : : | | | :|| :

Query Match Best Local Matches

1 Similarity
97; Conserv

Conservative

50;

129; 22;

Indels Length

147;

Gaps

20;

5.1%; 22.9%;

Score 124.5; DB 2 Pred. No. 0.00036; Mismatches

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AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress, CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. CC The C. glutamicum SRT genes (I) can be used in vectors (II) for C expression in host cells and production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a cc saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine chemical production can be modulated. The presence of (I) or the SRT cromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine corynchas (II) encoded by them are used for diagnosing the presence crowdens (II) encoded by them are used for diagnosing the presence crowdens (II) encoded by them are used for diagnosing the presence crowdens (II) or identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determination of SRT protein activity. Crowdens required for function, in modulating the SRT protein activity. Crowdens required for function, in modulating the SRT protein activity. Crowdens required for function, in modulating the SRT protein molecules convironmentally or chemically hazardous to it. (I) and protein molecules environmentally or chemically hazardous to it. (I) and protein molecules convironmentally are some survival of C. glutamicum to chemical and convironmental hazards and provide a means for continued growth and convironmental hazards and provide a means for continued growth and convironmental provide a means for continued growth and convironment to chemical strom a culture may be increased.
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08-JUL-1999;
08-JUL-1999;
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27-AUG-1999;
31-AUG-1999;
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Kim H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Corynebacterium glutamicum nucleic acid encoding a tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
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01-JUL-1999;
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06-NOV-1997;
14-NOV-1997;
18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
         Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis antigen encoded by ORF141.
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         sequences
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97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
98GB-0000759.
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  AAY38499-Y38944 represent Neisseria
                                               524pp; English.
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Best Local
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 01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy.
                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                             Neisseria meningitidis ORF 738 protein sequence SEQ ID NO:2518
                                                                                                                                                                                                                                                                             21-MAR-2000
                                                                                                                                                                                                                                                                                                              AAY75522;
                                                                                                                                                                                                                                                                                                                                           AAY75522 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAX11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                               30-APR-1999;
                                                                                                                          WO9957280-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GW-LPKLLAIAA-----TGASSLCLILTYSRGGWLGEVAMIEVWALLGLYWEQPRLPAPW 272
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98US-0094869.
98US-0098994.
                                                             99WO-US09346
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09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ5456 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
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Petersen Tettelin F
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391
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ictla
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                           MASLA 413
                                                     nllsnlft--hshnivlqllaemgisg-----tllvaatlltgiagllkrpltpaslfl
                                                                                LYQQARFTALSAYSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWL
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                                                                                                                                                                                                                                                  SRGGWLGEVAM-----IFVWALLGLYWE--QPRLPAPWRRWLEPVVLGGLVAVLLVAVL
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INST GENOMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used in gene therapy protocols.
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, Pizza M, Rappuoli
, Venter JC;
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20.5%;
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Rappuoli R,
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Pred. No. 0.00062;
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Scalato E,
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Scarselli
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Best Local Similarity 23.3
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06-NOV-1997;
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18-NOV-1997;
18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used their fragments, their nucleic acids and antibodies are used diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Bot organisms are closely related. Fragments of the nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequences AAY38499-Y38944 represent Neisseria menin and N. gonorrhoeae antigenic proteins. They are encoded by ope reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, the intigenic proteins, the continuous content of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY38797 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 340; 524pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-327407/27.
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202 YLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILTYSRGGWLGFVAMIFVWALLGL
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                                                                           fnflgrhhgrsvvliligcigliptvhflnpaaa...afaaaglvlhgyslarrrviaas
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                   CC This invention describes novel human and murine G-coupled receptors EDG CC (endothelial differentiation gene) 6 [I and II]. The products of the CC invention have antiinflammatory, immunomodulatory, antimicrobial, CC antiallergic and cytostatic activity. (I) and (II) are involved in signal CC transduction. (I), (II) and their fragments, variants and mutants or CC binding partners, are used therapeutically to modulate the function of CC blood and body cells, particularly for inhibition of acute and chronic CC inflammation and to raise specific antibodies against them. They are used CC as a source of diagnostic oligonucleotides and for gene therapy. CC when coupled to therapeutic agents, toxins or other antibodies, to CC modulate immune and inflammation, infection, autoimmune diseases, allergy, CC tumors, leukemia and lymphoma. This sequence represents the murine EDG6 cc protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human and murine G-coupled receptor EDG (endothelial differentiation gene) 6, useful for modulating inflammatory and immune reactions and for treatment of allergy or tumors
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Best Local S
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                                          02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
(CHIR )
                                                                                                   01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                        Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection;
                                                                                                                                      30-APR-1999;
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GENOMIC
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ż
                             AAG92136;
                                                        AAG92136 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2;
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n J, Pizza M,
n H, Venter JC;
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Rappuoli R,
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                   analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences from the Coryneform bacterium Corynebacterium glutamicum. I are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-2001.
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                                                                                                                                                                                                                                                                                                                                                                          European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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DB; AAH67355.
YLGNPNLLAAYLVPTT--
                                        glaasiklt pavfglyflvkk dwk gagvaias gvgfsalafllspssskiyw tetl ndps
                                                                                                                                                                                    FLLAVVY---GSAPFVP-----SSALGLGLAAIAA---YWA------LLSLTDIDLRQ 89
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                                                                                                                             ATPIHWLVLLYWGVDALATGLSPVRAAALVGLAKLTLYLLVFALAARVLRNPRL-RSLLF
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                                                                    SVVVITSLFVSVYGL----NQWIYGVEELATWVDRNSVA----DFTSRVY-----
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; 2000JP-0159162.
; 2000JP-0280988.
                                                                                                                                                                                                                                                                       Conservative
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Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis.
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Pred. No. 0.0027;
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Ozaki A;
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 Claim 11; Page 4966-4968;
                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant, cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hyportension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus crythematosus; infection; severa combined immunodeficiency.
                                                                                              N-PSDB; AAC77345
                                                                                                                                             Shimkets
                                                                                                            WPI; 2000-602362/57.
                                                                                                                                                                                                         30-MAR-2000;
                                                                                                                                                                                                                        02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                     31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                   05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       allergy; aplastic anaemia; nocturnal bone damage; cartilage damage; antii
                                                                                                                                                                                                                                                                                                                                                                                                                                                 severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORFX; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis; contraceptive.
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99US-0127728.
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5507pp;
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osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                   RLPAPWR-RWLFPVVLGGLVAVLLVAVLGLEPL 298
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                                                                                                                                    a \verb|mihvkrctpipallftcistllmlvtsdmytlinyvgfinylfygvtvagqivlrwkkp|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123; Indels 125;
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Search completed: January 10, 2002, 23:04:03 Job time: 2290 sec

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Copyright (c) 1993 - 2000
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probable inner mem	O-antigen ligase c	hypothetical prote	probable permease	NADH-ubiquinone ox	sodium/proton anti	probable Cynx-rela	hypothetical prote	probable drug tran	hypothetical prote	conserved hypothet	NADH dehydrogenase	nitrate transporte	NADH dehydrogenase	hypothetical prote	cationic amino aci

## ALIGNMENTS

hypothetical protein slr1515 - Synechocystis sp. (strain PCC 6803)
C.Species: Synechocystis sp.
A; Variety: PCC 6803
C.Species: PCC 6803
C.Species: PCC 6803
C.Species: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999
C.Accession: S75464
R; Kôneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys A; Status: preliminary A; Molecule type: DNA A; Residues: 1-474 <KAN> A;Cross-references: EMBL:D90911; A;Note: the nucleotide sequence v A; Reference number: S74322; SAYSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGM LAKLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRN VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVG
:: ||: : |:|| | ||: || | QSRGGWLAVLALGATFLALCYFWWLPQLPKFWQRWSLPLAIA--VAVILGGGALIAVEPI STLAQATRYYSFLGNPNLLAAYLVPMTGLSLSALVVWRRWWPKLLGATMVIVNLLCLFFT LAKLTANLCLFLLAARLLQNKQWLNRLVTVVLLVGLLVGSYGLRQQVDGVEQLATWNDPT 184 TSTIMLGIFMLLCGAFWALLTFADQPGKGLTPIHVLVFAYWCISAIAVGFSPVKMAAASG ISIWRSLMFGGFSPQEWGRGSVLHRLVGWGQSWIQASVLWPHFEALGTALVAIIFIAAPF Similarity Conservative BL:D90911; GB:AB001339; sequence was submitted 46.78; MUID:97061201 79; Score 1132; DB 2; Pred. No. 2.8e-73; '9; Mismatches 163; NID:g1653083; PIDN:BAA18025.1; PID:d101 to the EMBL Data Library, June 1996 Length 474; Indels 4. Gaps 418 362 358 302 298 244 240 180 124 120 64 Ŋ

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A; Molecule type: DNA
A; Residues: 1-438 <HEI>
A; Cross references: GB: AE004176; GI
A; Experimental source: serogroup O1
C; Genetics:
A; Gene: VC0931
A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                        FSLPLNQRASG-----SFVYHNHLANFL-MLNLCLGFGLLIAELNHQTTQ-----GWR
                                                                     SMTLPT
                                                                                                 WQPQPS 453
                                                                                                                            VTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTLWWLCIGAIASF 447
                                                                                                                                                                                                               DRPWLGIGPGNTAFNLVYPLYQQARFTAL--SAYSVPLEVAVEGGLLGLTAFAWLLLVTA
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  s1r0728
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24.7%; Pred. No. 1.7e-07;
tive 68; Mismatches 200
 Synechocystis
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C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text.
C:Accession: S74522
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; UDNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-387 < KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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LCLYNLFDVTIFDMRNNVLGWIFLAAIAGVSQRYGTK
                                             MLGHGLFDTVLYRPEASTLWWLCIGAIASFWQPQPSK 454
                                                                                                 MMLGETGLIGTALMLGAVGFILAQGMVLLI----HLSRGGGFRRRSQHLLLLSYGIAFAA
                                                                                                                                                 EVAVEGGLLG----LTAFAWLLLVTAVTAVRQVSRLRRD----RNPQAFWLMASLAGLAG
                                                                                                                                                                                                     LYPDRYRTALRSTQWQFSWDMFLDQPIFGQGLRNFT----PLYQAAMNVWIGHPHNLVL
                                                                                                                                                                                                                                                     ---EDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALS-AYSVPL
                                                                                                                                                                                                                                                                                                         YAIYLSWY--
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374
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vamada, M.; Yas
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MESOLIT 4

D82847

D82847

membrane protein XF0103 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82847
C;Accession: D82847
R;annoymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82847
A;Status: preliminary
A;Accession: D82847
A;Residues: 1-443 <SIN-
A;Residues: 1-443 <SIN-
A;Cross-references: GB:AE003864; GB:AE003849; NID:g9104879; PIDN:AAF82916.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carreras-
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreras-
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83368
R;Stover C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lari
A;Molecule type: DNA
A;Residues: 1-478 <STO>
A;Cross-references: GB:AE004649; GB:AE004091; NID:g9948246; PIDN:AAG05628.1; GSPDB:GN00:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2240
                                                                                                                                                                                                 Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337
A;Accession: A83368
A;Status: preliminary
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A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi Chado, M.A.; Madeira, A.M.B.N., Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes; L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa, J.Y. V.E.; de Sa, R.G.; Santelli, R.V.; Sawasah A.;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, R.M.; Silva Jr., W.A.; da Silvai, F.R.; da Silva, F.R.; da Silva,
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Best Local Similarity 25.2
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                       aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                  S.D.; Warrener, P.; Hickey, lger, K.R.; Kas, A.; Larbig,
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K.; Lim,
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RESULT 6
H75597
hypothetical
C;Species: De
                                                           A; Molecule type: DNA
A; Residues: 1-384 < WHI>
A; Cross-references: GB: AE001862;
A; Cross-references: Strain R1
A; Gene: DRA0046
A; Map position:
                                                                                                                                            A; Status: preliminary
                                                                                                                                                                A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Reference number: A75250; MUID:20036896 A;Accession: H75597
                                                                                                                                                                                                                              , M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                        R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald,
                                                                                                                                                                                                                                                                                                               C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C;Accession: H75597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHGLEDTVL-YRPEASTLWWLCIG-----AIASFWQPQP-----SKQLPPEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILTYSRGGWLGFVAMIFVWALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSGLEDHYESFAVVMIGLEWLLVGINLLEARRLFPERQPQPRAVGYRKLKRQLERGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVGL-GGMLLFIAVTW------RWWREARPEKGPIRLTRDNAIWL-GSTGGILAAL 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVAVEGGLIGLTAFAWLLLVTAVTAVRQVSRLRRDRNP-----QAFWLMASLAGLAGML 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYWFQPRLPAPWRRWLFPVVLG-GLVAVLLVAVLGLEPLRVRVLSIFVGREDSSNNFRIN 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLLPLAFCYGVANQGWRRGLG--LAVAVLGAAA--ILLASSRGAMLSLAVVLF-WMSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYRMFPKAVARYP-LGIGFKVDPPVPGTDLLGISNLWLNFMY---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VWLAVLQMIQDRPWLGIG------PG-----NTAFNLVYPLYQQARFTALSAYSVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVSIKAEASGLSNWLRWLLNLSIVFLAGRLLVERKNRETLVIALLLGTLAMLLMSIAVFI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYRSASGMAPILAMFNYANLDTLKFGLEAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNVGIR-STVSEAILALTWGAVLWHIFLSRLPPAPALRYRSTERMLLWLMLFTVLPFVVG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFLLAVVYGSA-------PFVPSSALGLGLAAIAA----YWALL-----
                                                                                                                                                                                                                                                                                                                                                                             protein - Deinococcus radiodurans (strain RI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GLNQWIYGVEELATWVDRNSVADFTSRVYSYLGNPNL---LA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LLLGVGLVVVL----VLSYPPLQERLATIF-SPQNASTEVRFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 180; DB 2; 23.0%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Mismatches 159;
                                                                             GB:AE001825; NID:g6460468; PIDN:AAF12372.1; PID:g646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LAARVL----RNPRLRSLLFSVVVITSLFVSVY-
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                                                                                                                                                                                                                                                                                                                                   #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                   E.K.; Peterson,
L.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 478;
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                                                                                                                                                                                                                                                                     J.D.; Dodson,
T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SL
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C; Genetics:
A; Gene: VC0393
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-597 <HBI>
A; Cross-references: GB:AE004127;
A; Experimental source: serogroup
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein VC0393 [imported] - Vibrio cholerae (strain N16961 ser C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82328
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;
Chardson, D.; Ermolaeva, M.D.; Venathevan, J.; Bass, S.; Qin, H.; Dragoi, I
L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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Best Local S
Matches 109
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVAVLLVAV-LGLEPLRVRVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y---TLST----QGVAGVQERLGHPYYYIVSLGLVAVVALWIVMFWRGAAAWWR-WPAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAIAATGASSLCLILTYSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRW-LFPVVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGLV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLVTAVTAVROVSRLRRDRNPQAFWLMASLAGLAGMLGHGLFDTVLY - - RPEASTLWWLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYLTYLFKDGCQLTPTLQRNKIECPQQLSRWSSVWLIAHNAWLHWLLESGIIGLSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNLVY------PLYQQ------ARFTA--LSAYSVPLEVAVEGGLLGLTAFAWL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAAFATTSLNVPFKPLDRLLNDQTSGRE-----YVWQDAVSGWETSPLGGVGPYQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGVEELATWVDRNSVADFTSRV---YSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFTPAPLLSVGLAAARTLLILAMVAAGVYLRDSRHLRPLLWGQLII---FVTA----WI
 FVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRVRVLSIFVGREDSS
                                                                                                                                                LWLSCALLT - - LPITYSNADWFHTLGRLVGLWAGFTLFLVLQQF - - RFSNKHKQRLLWF -
                                                                                                                                                                             YWGVDALATGLSPV------RAAALVGL-AKLTLYLLVFALAARVLRNPRLRSLLFS 149
                                                                                                                                                                                                                                   FLLAVVYGSAP--FVPS-SALGLGLAAIAAYWALLSLT-----DIDLRQATPIHWLVLL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGAI 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLAIMVYALWRAIQL---GDP-----FTLAVLYGFTAMNVVDVVIAVPSPHFSELWWVC
                               LVLS---
                                                           TAFSAAAIGVWRGWL---
                                                                                     -ILLGSVIEAVIGLIQYF-----
                                                                                                                   VVVITSLFVSVYGLNQWIYGVEELATWVDRNSVADF---TSRVYSYLGNPNLLAAYLVPT
                                                                                                                                                                                                         FALAVVYLLAMHFFMPNPGGAGLALSFNTTVWIATSITLAIGLYQLANNQALRYSKLTIG
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TFAAAGSRGPLLALGVGSLAALAFGGQRR----RVWVMLPAVLVM
                            -GYLLARQPEKYDSRWSKIGILYATPLLTAPLLVVLASRTGWLASLLSI
                                                                                                                                                                                                                                                                              6.9%;
                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                  GB:AE003852; NID:g9654808; PIDN:AAF93566.1; GSPDB:GN00:
O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                Score 166.5; DB 2;
Pred. No. 0.00015;
0; Mismatches 185;
                                                                                        WLEPGNPFGYDTEANRPYGIFQQPNVMASFLATG
                                                         -PKLLAIAATG-ASSLCLILTYSRGGWLGFVAMI
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen Vibrio cholerae
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                                                                                                                                                                                                                                                                                                597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                  95;
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                               246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                               TAVTAVRQVSRLRRDRNPQ---
                                                                                                                                                                                                                                        ILELQNWAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S77086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.6%;
22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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$77086
hypothetical protein sl10737 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A; Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: $77086
C;Accession: $77086
R; Kaneko, T; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; I
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamad
DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA10778.1; PID:g100 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: Synechocystis hypothetical protein s110737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown;
A;Molecule type: DNA
A;Residues: 1-861 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 VEELATWVDRNSVADFTSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVW-----RGWLPKL
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                                                                                                                                                                    PWLGIGPGNTAFNLYYPLY------QQARFTALSAYSVPLEVAVEGGLLGLTAFAWLLLV 385
                                                                                                                                                                                                                                                                                       GGLVAVLLVAVLGL-EPLRVRVLSIFVGREDSSN-----NFRINVWLAVLQMIQDR
                                                                                                                                                                                                                                                                                                                                                    ----ALSLGLIDFYTTSSRGGLLG-LATLLLLVIIGIGLLR---QLPWRWWL-----
                                                                                                                                                                                                                                                                                                                                                                                           LAIAATGASSLCLI---LTYSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KVQTNPLVSINKLLTFQGYVGFAFIVISLLLWFTQTLIPFWQSAAIAREMGITKTFTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFILLAVVYGSAPFVPSS-ALGLG-------LAAIAAYW-----ALLSLTDIDLR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEDTVLYRPEASTLWWLCIGAIASFWQPQ 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLYYPLYQQARFTALSAYSVPLEV-----
PSLLIIGLIWQLIRSLIKQNIVNTKGNDVDSNVVKILIWTLTS ----ALLAYGVTSLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARVLRNP--RLRSLL-----FSVVVITSLFVSVYGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GLGFDWLMVAL----AIAAMLSVVGAEFPQQARWYGWIFCAFLAGLYGLRSWL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QATPIHWLVLLYWGVDALATGLSPVRA·····-AALVGLAKLTLYLLVFALA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLLTALLYGLFTLLPNGHSLMVGWPWVFVWQTWFWLTALWCLWQIGQNKRLISL-----
                                                                                                             PWTGIGLGNVP--LQYQLYRPVWAGRESEF-IYQLHSTPAQLFAELGV------WGILI
                                                                                                                                                                                                                                   -GL-GTLAIAVVGIFICTNDRLLTSFTGIMGGQGAGQFAYRLINFEIG-W----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----IGHQNYVAGYLV--LILPLLSVLIWLNEGKKRWFWSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 159; DB 2;
Pred. No. 0.00073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation
                                                         -AFWLMASLAGLAGMLGHGLFDTVL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145;
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pabe, A.; Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NOWIYG
                                                                                                                                                                                                                                       RMGSAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y.; Miyajima,
Yamada, M.; Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422
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   434
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hypothetical protein PA0345 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G83602 C;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
B83022
hypothetical protein PA4999 [imported] - Pseudomonas aeruginosa (strain PAO)
C;Species: Pseudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-401 <STO>
A;Cross-references: GB:AE004912; GB:AE004091; NID:g9951274; PIDN:AAG08384.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337 A;Accession: D83022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, i. Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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Best Local S
Matches 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 24.3 mes 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y-MMLSLS----
                                                                                                                                                                                                                                                ASLAGLAGMLGHGLFDTVLYRPEASTLW---WLCIGAIASFWQPQ
                                                                                                                                                                                                                                                                                           GMLLADPHNIELGVLFAGGIIG-
                                                                                                                                                                                                                                                                                                                                                                                                              RVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVGLAKLTLY--LLVFAL 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVGDRSDYHRLFYILLA--APTLLYV---ILQPRLLRPLTGSPLFI------AFLAFSS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQLDN----VCISGV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRPEASTLWWLCIGAI 444
                                                                                                                                                                                                             FGLAA---
                                                                                                                                                                                                                                                                                                                                ----AYSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAF----WLM 409
                                                                                                                                                                                                                                                                                                                                                                         RGAS-----YDHPMRIVLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSRTPLVGLTAAL-MWLVLA------GDRKKALIALAL-ALAGALLGYILYPEVITQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSRGGWLGFYAMIFYWALLGLYWFQPRLPAPWRRWLFPVVLGGLYAVLLVAVLGLEPLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLTGYGALYNP-LLSAHVY--GAFTALWLAYWMQSRPILAPLPLISLALLGG----LLIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RV--YSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLP-----KLLAIAATGASSLCLILT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AILALEAPLRIKTATWIAALGAVISAAATIIRYY------W-DANPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AARVLRNP-RLR-----SLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRNSVADFTS 187
                                                                                                                                                                                                             -GLTEGNAFLPRPKEHWFLIWIPMALLYALWIQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 151.5; DB 24.3%; Pred. No. 0.0011; rative 53; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----WSTPENSTG-----SLLKRPLYIALLFFCA 115
                                                                                                                                                                                                                                                                                           - LLLWVAIYALAFGFSWKNRKSPAVLLASTWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Warrener, P.;
K.R.; Kas, A.;
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Larbig,
                                                                                                                                                                                                                                                                                           349
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K.; Li
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; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic |
A;Reference number: A82950; MUID:20437337

A;Accession: G83602

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <5TOO
A;Cross-references: GB:AE004472; GB:AE004091; NID:g994618B; PIDN:AAG03734.1; GSPDB:(A;Experimental source: strain PA01
A;Experimental source: strain PA01
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                                  Q
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Best Local (
420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLLVFALAARVLRNPRLRSLLFSVVVIT-----SLFVSVYGLNQWIYGVEELATWVD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDGQRPVNVFWALASLLG------LHLLTLLGWALGLLAGG----EAAGALG--RLWL
                                                                        RLLEQUTRYPPARLAIACDPRRSPD-----
                                                                                                              AWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTLWWL 439
                                                                                                                                                    LVAVELDDRRPW----PPKLA--
                                                                                                                                                                                                                                                  LGGLVAVLLVAVLGLEPLRVRVL--SIFVGREDSSNNFRINVWL---
                                                                                                                                                                                                                                                                                                                                                                               ---LGLLATRRYGEVWETTILGSDTFIALTQALGA------LPALLGFPLPDAELIR
                                                                                                                                                                                                                                                                                                                                                                                                                 RNSVADFTSRVYSYLGNPNLLAA--YLVPTTAFSAAAIGVWRGWLPKLLA-----IA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W-----LSGKLARDARAAHLAPALLVLLGRRRLARWGLGALVHGL--WLLGLLTALAML-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVGLAKLTL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTRAHWLGRREG - - - - - - LLDALRTWRQGSRLAL - - - - - ALLLYLALASGAGLAFAAL
                                  CIGAIASFWQPQPSKQLPP-EAEHSD 464
                                                                                                                                                                                      LQMIQ----DRPWLGIGPGNTAFNLVYPLYQQARFTALSAYSVPLEVAVEGGLL--GLTAF 379
                                                                                                                                                                                                                                                                                                       ASGDAALA--SEAARHAWAGWLVGVLLVYGVLPRALLGLLCLW-----RWKRGLAHLD 292
                                                                                                                                                                                                                            LD-----LDDPGYSLLRERLMPASERLGVSDAAPD-----WLPEPQGGQSGQEAAGAV
                                                                                                                                                                                                                                                                                                                                       ATGASSLCLILTYSRGGWLGF-VAMIFVW-----ALLGL--YWFQPRLPAPWRRWLFPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
120; Conserv
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23.7%;
QAPPGEALDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 151.5; DB pred. No. 0.0013;
  431
                                                                            -RGTLALLGE---
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                                                                                                                                                    -EGVADAGILDDGQQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
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                                                                            --LARCAASTRIWL
                                                                                                                                                                                                                                                                    ----AV
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RESULT 11

G75375
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: G75375
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu
A;Reference number: A75250; MUID:20036896
A;Accession: G75375
A;Status: preliminary
A;Status: preliminary
A;Accession: NNA
A; Molecule type: DNA
A; Residues: 1-388 <WHI>
A; Cross-references: GB:
GB:AE002004; GB:AE000513; NID:g6459366;
       PIDN: AAF11168.1;
                                                                                                                                                                                                                                                                                                                                 J.D.; Dodson,
T.; Zalewski,
                                                                                                                                                                                                                            radiodurans
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PID:9645

**R**1

R.J

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A; Experimental source: strain C; Genetics: AR1602 A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable LPS biosynthesis enzyme waaL [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E86038
C;Accession: E86038
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheviller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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C;Genetics:
A;Gene: waaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E86038
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A; Residues: 1-402 <S
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Best Local Similarity 28.4
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 VL--RNPRLRSLLFSV-VVITSLFVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 ------ESANPVQYLNDALLSAWGLRGL---LSVVPTTALV-------LLGALAAR
  239 L-TYSRGGWLGEVAMIEVWALLGLYWFQPRLPAPWRRWLEPVVLGGLVAVLLVAVLGLEP
                                                   164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 GKSQSIAAS------LLEMARSSFGPVGGGWTYTLGYV--FAVW--LGLAWMARR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 PKLLAIAATGASSLCLILTYSR------GGW---LGFVAMIFVWALLGLYWFQPR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.8
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nes 85; Conserv
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                                                                                                                                                                                                                                   46 MTTTTIVYLCKRPKHYLSLEKTFLFGSVAILTIAALLSLLQSPDAGASMKEIFKAIIENT
                                                                                                                                                                                                                                                                                 80 LSLTDIDLRQATPIHWLVL----LYWGVDALATGL-----SPVRAAALVGLAKLTL-YL 128
                                                                                                                                                                                                                                                                                                                                                                            26 LFGSL--RAWRASSQLLVWSEALGGFLLAVVYGSAPFVPSSALGLGLAAIAAY----WAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLQQKNPRAPLLLLGLGVVLTALGYGWAASGRLPFSKALWTPPYILYSAGLGTLGI--LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CWV----VADSGWLPGGKRLLAPLTIPGRNALAGYVLP-----ILIKVWILLDWQVGWT
                                                R-SISD--SMVFLF---PALLNLWLIKSAKYR---
                                                                                               RNSVADFTSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLI 238
                                                                                                                                           LLCTIAIPIILRDEKREDVEKIVFFS--FISALGLRCFSELITYYKDYQQGIMPFADYRH 163
                                                                                                                                                                                       LVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGL-------NQWIYGVEELATWVD
                                                                                                                                                                                                                                                                                                                                  LFFSLEKKNW----IAYWNRAL-VFLFITTY--
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 138.5; DB 2;
21.8%; Pred. No. 0.0096;
'ative 67; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 139.5; DB 2; Length 388; 28.4%; Pred. No. 0.0079; ative 24; Mismatches 81; Indels 107;
                                                   -----ISFVVLSVIFIFLI
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                                                                                                                                                                                                                                                                                                                                  ---FLGGITRYKHLIVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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       297
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RESULT
G75267
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A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Reference number: A75250; MUID:20036896
A;Accession: G75267
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A;Map position: 1
C;Superfamily: sfuB protein
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A;Residues: I-515 <WHIST
A;Cross-references: GB:AE002078; GB:AE000513; NID:g6460306; PIDN:AAF12029.1;
A;Experimental source: strain R1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABC transporter, permease protein, CysTW family - Deinococcus radiodurans (strain C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: G75267
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Best Local Similarity
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458
                                                                               400
                                                                                                                                                                                                                                               305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 RF-TALSAYSVPLEVAVEGGLLGLTAFAWL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 EMTAKLTYKLQQTNSSYRYANGTQGSALDLILENPVIGYGYGNVAYKDVYNKRVIDYPEW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                      424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 LLVWSEALGGF--LLAVVYGSAPFVPSSALG----LGLAAIAAYWALLSLTDIDLRQATP 92
                                                                                                                                                                  LYALGAWLARSRVLDLISLLP-LMVSPVSLAVGYLLAYPVLAATLPMLIAAYTLLALPLL
                                                                                                                                                                                                                                                 LLYW-------RGVVNDEQTPLLLGNTLRFGALALLGATAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLAAGAVLVFLY---SALSFGL----PLALGGERYATLEVEIYTLTALQLRLPEASALIV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----IHWLVLLYWGVDALATGLSPVRAAALVGLAKLTLYLLVFALAARVLRNPRLRSLLF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TERQSIGPHNEALFIWEGTGLLGLVSLMML
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                                    FDTVLYRPEASTL 436
                                                                           VRSLLPALRAIPPRLFEAARTL--GASPLAAHRTVTLPLTLPALRGGAALALATVLGEFG
                                                                                                                                                                                                      NFRINVWLA---VLQMIQDRPWLGIGPGNTA--FNLVYPLYQQARFTALSAYS-VPLEVA 368
                                                                                                                                                                                                                                                                                    -LYWFQPRLPAPWRRWLF-----PVVLGGLVAVLLVAVLGLEPLRVRVLSIFVGREDSSN 314
                                                                                                                                                                                                                                                                                                                                 LTRGGAGVATGGLPRARGGALAGITLLGGLTLLVCFAP - - - - - - LLAVVVVRGLVGSAGPT
                                                                                                                                                                                                                                                                                                                                                                        FSAAAIGVWRGWLPKLLAIAATGAS---SLCLILTYSRGGWLGFVAMIFVWALLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVVVITSLFVSVYGLNQWIYGVEELATWVDRNSVADFTSRVYSYLGNPNLLAAYLVPTTA 208
                                                                                                                    VEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAG-----LAGMLGHGL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRVRVLSIFVGREDSSNNFRINVWLAVLOMIODRPWLGIGPGNTAFNLVYPL----YQQA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 51; Mismatches 154; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                 --VATWL---
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Pred. No. 0.013;
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T.; Zalewski,
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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresist A: Reference number: A75250; MUID:20036896
A;Accession: H75389
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Deinoco C. Species: Deinococcus radiodurans C. Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000 C. Accession: H75389 J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D. R. White, O.; Eisen, J.A.; Heidelberg, J. R. White, O.; Eisen, J. R. White, O.; Eisen, J. R. White, D. R. White, O.; Eisen, J. R. White, D. R
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H75389
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-443 <STO>
A;Cross references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04597.1; GSPDB:GN0C
A;Experimental source: strain C-125
C;Genetics:
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C;Superfamily:
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314
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Pred. No. 0.012;
1; Mismatches 129;
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A;Residues: 1-474 <WHI>
A;Cross-references: GB:AE001993; GB:AE000513; NID:g6459244; PIDN:AAF11056.1;
A;Experimental source: strain R1
C;Genetics: A;Gene: DR1493
A;Gene: DR1493
A;Map position: 1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; NAD; oxidoreductase
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                                                                                             MASLA--GLAGMLGHGLFDTVLYRPEASTLWWL---
                                                                                                                              -ETAVIGAMY-LLAFQNLYTGALFMAVGMLQERVGSLDTRVGGVMNQAGALGGLTLALW-
                                                                                                                                                              LEVAVEGGLLGLTAFAWLLLVTAVTAVRQV-----SRLRRDRNPQ-----AFWL 408
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Search completed: January 10, 2002, 23:11:14 Job time: 381 sec

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YHHS_ECOLI
POTE_ECOLI
POTE_ECOLI
CATT_ECOLI
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YFB1_ECOLI
POLG_HCYH
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FERRICHROME TRANSPORT SYSTEM PERMEASE PROTEIN
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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Fujita N., Mori H., Yura T., Ishihama A.;
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the 2.4-4.1 min (110,917-193,643 bp) region.";
Nucleic Acids Res. 22:1637-1639(1994).
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"Iron hydroxamate transport of Escherichia coli: nucleotide sequence of the fhuB gene and identification of the protein.";
Mol. Gen. Genet. 204:435-442(1986).
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Query Match Best Local S Matches

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BL; U70214; AAB08583.1; -.
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R; S07318; S07318; R; S45222; S45222.
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FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED AFFINITY TRANSPORT OF IRON(III)-FERRICHROME INT
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FecCD_family;
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D., Namath A., Oefner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92041612; PubMed-1657881;
Maclachlan P.R., Kadam S.K., Sanderson K.E.;
"Cloning, characterization, and DNA sequence of the rfalk region lipopolysaccharide synthesis in Salmonella typhimurium LT2.";
J. Bacteriol. 173:7151-7163(1991).
J. Bacteriol. 173:7151-7163(1991).
J. PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
                                                                           Lipopolysaccharide
TRANSMEM 66
                                                                                                                                                                         EMBL; M73826; AAA27206.1;
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P33608; P78281;
01-FEB-1994 (Rel. 28
01-NOV-1997 (Rel. 35
20-AUG-2001 (Rel. 40
NADH DEHYDROGENASE I
MEDLINE=97349980; PubMed=9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kitura S., Kitagawa M., Makino K., Miki T., Mitsuhashi
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram
                                                                                                                                                                                                                                                                           MEDLINE-93389724; PubMed-7690854; Weidner U., Geier S., Ptock A., Friedrich T., Leif H., Weiss "The gene locus of the proton-translocating NADH: ubiquinone oxidoreductase in Escherichia coli. Organization of the 14 general
                                                                                                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose E Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB 1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NADH DEHYDROGENASE I CHAIN N (EC 1.6.5.3) (NADH-UBIQUINONE
OXIDOREDUCTASE CHAIN N) (NUO14).
NUON OR B2276 OR Z3534 OR ECS3160.
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MEDLINE=97426617; PubMed=9278503;
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MEDLINE=93389724; P:
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233:109-122(1993).
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Pred. No. 0.
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OXIDOREGUCTASE;
TRANSMEM 11
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TRANSMEM 67
TRANSMEM 143
TRANSMEM 175
TRANSMEM 211
TRANSMEM 211
TRANSMEM 237
TRANSMEM 237
TRANSMEM 335
TRANSMEM 313
TRANSMEM 313
TRANSMEM 395
CONFLICT 63
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"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA RES. 8:11-22(2001).

THE IMMEDIATE ELECTRON FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINORE. DOES COUPLE THE REDOX REACTION TO PROTON TRANSLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
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Vamaqata S., Horiuchi T
                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apodaca J., Anantharaman T.S., Lin J., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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STRAIN=0157:H7 / 1
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                                                                                                                                                                                                                                                                                                             EMBL;
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MEDLINE-21156231; PubMed=11258796;
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European Bioinformatics Institute.
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SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
                                                                                                                                                                                                                                                                                S38323;
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                 REF. 1).
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P39879; Q9I289;
01-FEB-1995 (Rel
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STRAIN-ATCC 15692 / PAO1:

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _PSEAE
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20-AUG-2001 (Rel. 40,
20-AUG-2001 (Rel. 40,
                                                    Perry A.C.F., Bhriain N.N., Brown N.L., Rouch D.A.;
"Molecular characterization of the gor gene encoding glutathione reductase from Pseudomonas aeruginosa: determinants of substrate specificity among pyridine nucleotide-disulphide oxidoreductases.
MOL. Microbiol. 5:163-171(1991).
                                                                                                                                                    SEQUENCE OF
STRAIN=PAO8;
                                                                                                                                                                                           "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
nature 406:959-964(2000).
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                          MEDLINE=91194546; PubMed-1849605;
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
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              MEDLINE-99310339; PubMed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamara Y., Nomura N., Sako Y., Kikuchi H.;
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AERPE
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Archaea; Crenarchaeota;
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30-MAY-2000
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EMBL; X54201; CAA38123.1;
PIR; S15237; S15237
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hyper-thermophilic
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InterPro; IPR000298; CyCC_oxdse_III.
Pfam; PF00115; COX1; 1.
Pfam; PF00510; COX3; 1.
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DNA Res. 6:83-101(1999).
-!- COFACTOR: TWO HEME GROUPS AND COPPER B (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE H
            146
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EMBL; AP000060; BAA79771.1; ALT_INIT.
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                          YEAVTVHGLIMLLWFASPFAFGLAN------YIVPLQTGARDLAFPRLNALS
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
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NU4M_ST
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DT 01-FBR
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DT 01-FBR
DT 01-FBR
DT 20-AUG
GN NUAH-U
GN NUAH-U
GN NUAH-U
CC Eukary
OC OT ST
NO1
CC -1- CA
CC -1- CA
CC -1- CA
CC This S
CC Use b
CC Use b
CC Use b
CC OT Sen
CC OT Sen
CC OT Sen
DR Interp
DR Pfam;
SQ SEQUEN
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01-FEB-1996
20-AUG-2001
                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89011951; PubMed-3172215;
Jacobs H.T., Elliott D.J., Math V.B., Farquharson
"Nucleotide sequence and gene organization of sea
mitochondrial DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Echinoidea; Strongyloce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NU4M_STRPU
P15551;
                                                                                                                                                                                                              EMBL; x12631; CAA31159.2; -.
PIR; S01508; S01508.
InterPro; IPR003918; NADHub_oxdrdctse4
                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus (Purple sea urchin).
                                                                                                                            Oxidoreductase; NAD; Ubiquinone; Mitochondrion. SEQUENCE 463 AA; 50507 MW; 5C8E73FE7D5CAAF0
                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol.
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19
                          61 VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHW-----
                                                                                                                                                                                                                                                                                                                                                                                  Mol. Biol. 202:185-217(1988).
CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
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 IPSNKLWAGAIFQSALLSLIVLN----
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                                                                                                                                                     PF00361; oxidored_q1; 1.
PF01059; oxidored_q5_N; 1.
                                                        90;
                                                                     Similarity
                                                                                                                                                                                   IPR001750; Oxidored_q1.
IPR000260; Oxidored_q5_
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                  18.8%;
                                                     52;
                                                                    Score 119; DB Pred. No. 0.73;
                                                                                                                                                                                 1_q5_N.
                                                        Mismatches 132;
-NHWTASWHNLSSILASDTISAPLIILSC
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                                                                                   Length 463
                                                                                                                              CRC64;
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                                                        Indels
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                                                         17;
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    RESULT 8
Y608_HAEIN
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                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q57486;
01-NOV-1997
              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-RD
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae
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  U32743;
HI0608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                       KW20 / ATCC 51907;
              AAC22267.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma
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MEDLINE-9535630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriges T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN HI0608.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGVDALATGLSPVRAAALVGL------AKLTLYLLVFALAARVLRNPRLRSLLFSVVV
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|----LKALIAYSSVGHMSIVAAAIFSETSWGMNGALMLM
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Pfam; InterPro;

PF00939;

IPR001898; Na\_sulph\_symp.

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Best Local Sin
Matches 110;
                                                            HUMAN

LAT2_HUMAN

STANDARD;

PRT; 535 AA.

99UHI5; Q9Y445; Q9UKQ6; Q9UKQ7; Q9UKQ8;

20-AUG-2001 (Rel. 40, Created)

20-AUG-2001 (Rel. 40, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

LARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL SUBUNIT 2

ACID TRANSPORTER 2).
                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
SEQUENCE FROM
                   NCBI_TaxID=9606,
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TRANSMEM
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                                                                                                                                                                                                                    WLMASIAGLAGMIGHGLFDTVLYRPEASTLWWLCIGAIASFWQPQPSKQLPPEA 460
                                                                                                                                                                                               LLVPIFISIAQSLG------MPEIGLALIIGIGASCAFMLPVAT---PPNA 423
                                                                                                                                                                                                                                                              YQQARFTALSAYSVPLEVAVEGG----LLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAF
                                                                                                                                                                                                                                                                                                      ---PLRVRVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGI---
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                                                                                                                                                                                                                                                                                                                                                                                                 PTTAFSAA--AIGVWRGWLPKLLAIAATGASSLCLILTYSRGGWLGFVAMIFVWAL-LGL
                                                                                                                                                                                                                                                                                                                                                                                                                                            SLFVSVYGLNQWIYGVEELA-----TWVDRNSVADFTSRVYSYLGNPNLLAAYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLSPVRA-AALVGLAKLTLYLLV--FALAA-----RVLRNPRL---RSLLFSVVVIT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFFVLLNVLPFEPKANSGLALLAFIAVLW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLAVVYGSAPFVPSSALGIGLAA-IAAYWALLSITDIDLRQATPIHWLVLLYWGVDALAT 108
                                                                                                                                                                                                                                           LKDSGASKILADSIVF--MIDGQHFYLIGLLVAAFIIFLTEFTS---
                                                                                                                                                                                                                                                                                     ASFDSIVALLAAIV-----ICSTGVASWKQIQSNTDWGVLMLFGGGLT---
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71; NA_SULFATE;
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                              Craniata; Vertebrata; Catarrhini; Hominidae;
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                              Euteleostomi; Homo.
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of kidney and J. Biol. Chem. [2]
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Lloberas J., Zorzano A., Palacin M.;
"Identification of a membrane protein, LAT-2, that
4F2 heavy chain, an L-type amino acid transport act
specificity for small and large zwitterionic amino
J. Biol. Chem. 274:19738-19744(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sebastio "SLC7A7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "SLC7A7, encoding a putative permease-relate patients with lysinuric protein intolerance. Nat. Genet. 21:297-301(1999).
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Borsani G., Bassi M.T., Sperandeo;
Riboni M., Manzoni M., Incerti B.,
Sebastio G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCDLINE=20044753; PubMed-10574970;
ROSSIer G., Meier C., Bauch C., Summa V., Sordat B.,
Kuhn L.C.;
"LAT2, a new basolateral 4F2hc/CD98-associated amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPORT PROTEIN SLC3A2/4F2HC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
TISSUE SPECIFICITY: MAINLY EXPRESSED IN KIDNEY AND INTESTINE.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
PERMESSES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOL. Chem. 274:19738-19744(1999).

BIOL. Chem. 274:19738-19744(1999).

BUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE NEUTRAL AMINO ACIDS. HAS HIGHER AFFINITY FOR L-PHENYLALANINE THAT LATI. L-ALANINE IS TRANSPORTED AT PHYSIOLOGICAL CONCENTRATIONS.

PLAYS A ROLE IN BASOLATERAL (RE)ABSORPTION OF NEUTRAL AMINO ACIDS.

SUBUNIT: DISULFIDE-LINKED HETERODIMER WITH THE AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY.
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, Andria G., Ballabio A.
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entities requires a license agreement (Some send an email to license@isb-sib.ch). use by non-profit institutions as long modified and this statement is not removed. the s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is AF135830; AAF05697.1; -. AF135829; AAF05696.1; -. AF135828; AAF05695.1; -. license agreement (See http://www.isb-sib.ch/announce/ . Usage γd restrictions and for collaboration outstation in no 9

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Transport; Amino-acid\_transport; Transmembrane. InterPro; InterPro; MIM; 604235; IPR002293; IPR002027; 1133 1133 175 209 251 288 330 330 267 464 468 58381 Amino\_acid\_permease. AA\_rel\_permease\_1. W. POTENTIAL
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Best Local
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F73182;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
20-AUG-2001
                                                                                                                                                              Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis NCBI_TaxID=1148;
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                                                                                                                                                                                                                                                                                                                                        FEOB OR SLR1392.
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                                  EMBL; D90904; BAA17208.1; -.
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed-8905231;
                     InterPro; IPR003373; FeoB.
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                                                                                    ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no re by non-profit institutions as long as its conten
                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
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 transport;
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            PF02421;
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01-FEB-1994 (Rel. 2
20-AUG-2001 (Rel. 4
CYTOCHROME C-TYPE E
CCMF OR B2196
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P33927;
01-FEB-1994
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InterPro; IPR003567; Cyt_c_biog.
Pfam; PF01578; CytC_asm; 1.
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Blattner F.R., Plunkett G. III, Bloch C.A., Perr
Riley M., Collado-Vides J., Glasner J.D., Rode (
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome c-type biogenesis; Transmembrane; Inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
VAFAFAIASLLSGRLDSTYARFT-----RPWTLAAWIFLTLGIVLGSAWAYYELG-W
                                                                                   QLPVWYRVAATWG-----AHEGSLLLWVLLMSGWTFAVAIFSQRIPLDIVARVLAIM
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                                                                                                                             VYPLWGVARGDARMMASSRLFAWLLFMSVAGAFLVLV----NAFVVNDFTVTYVASNSNT 77
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                    -QWIYGVEELATWVDRNSVADFTSRVYSYLGNPNLLAAYLVPT----TAFSAAAIGVW
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Rhizobiaceae; Rhizobium.
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STRAIN-RCR2011 / SU47;
MEDLINE-93177026; PubMed-8439670;
MUELLE-93, Keller M., Weng W.M., Quandt J., Arnold W., Puchler Mueller P., Keller M., Weng W.M., Quandt J., Arnold W., Puchler "Genetic analysis of the Rhizobium meliloti exoYFQ operon: ExoY."
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01-OCT-1996 (Rel. 34, Createu,
01-OCT-1996 (Rel. 34, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
CYTOCHROME C-TYPE BIOGENESIS PROTEIN (
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SEQUENCE FROM N.A
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                                    Bacteria; P
Pseudomonas
                                                                                                                                                        CCMF_PSEFL
                        NCBI_TaxID=294;
                                                              Pseudomonas fluorescens.
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Pred. No. 0.73;
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                                                   Pseudomonadaceae;
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: REQUIRED FOR THE BIOGENESIS OF C-TYPE CYTOCHROMES.
POSSIBLE SUBUNIT OF A HEME LYASE (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
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the European Bioinformatics Institute.
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YPLYQQARFTALSAYSYPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAF
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                                                              VLLVAVLGLEPLRVRVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLV
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IPR003567; Cyt_c_biog.
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hilarity 20.3%;
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                               --GSLTLFVRAPVVKSQVGFNLWSRETLLLGNNLVLVVAASMILLGTL
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Pred. No. 1.4;
58; Mismatches
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Query Match Best Local S Matches 85

Similarity

4.8%; Score 116; Dilarity 22.5%; Pred. No. 1.3 Conservative 54; Mismatches

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MEDLINE-99321902; PubMed=10391916;

MEDLINE-99321902; Myamoto K., Takeda E., Endou H., Kanai Y.;

Segawa H., Fukasawa Y., Miyamoto K., Takeda E., Endou H., Kanai Y.;

"Identification and functional characterization of a Na+-independent neutral amino acid transporter with broad substrate selectivity.";

J. Biol. Chem. 274:19745-19751(1999).

-i- FUNCTION: SODIUM-INDEPENDENT, HIGH-AFFINITY TRANSPORT OF LARGE NEUTRAL AMINO ACIDS. HAS HIGHER AFFINITY FOR L-PHENYLALANINE THANNEUTRAL AMINO ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9WVR6;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
1.ARGE NEUTRAL AMINO ACIDS TRANSPORTER SMALL S
 SEQUENCE
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InterPro; IPR002027; Amino_acid_permease.
Pfam; PF00324; aa_permeases; 1.
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                                                                                                                                                                                                                                                                                                                  EMBL; AB024400; BAA82517.1;
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Rattus norvegicus (Rat).
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Mammalia; Eutheria; Rodentia;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
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Sciurognathi; Muridae;
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99479DB60DA69DF0 CRC64;
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DЬ	Qγ	дb	Qy	Ф	Qy	밁	Qy	Db	Qy	ф	Qy	рь	Qγ
432	282	372	230	334	182	276	124	216	110	161	65	102	14
432 LLFWAFLLIFSLWSEPV 448	GGLVAVLLVAVLGLEPL 298	TCLSTLLMLVTSDMYTLINYVGFINYLFYGVTVAGQIVLRWKKPDIPRPIKISLLFPIIY 431	TGASSLCLILTYSRGGWLGFYAMIFVWALLGLYWFQPRLPAPWR-RWLFPVVL 281	SLFTSSRLFFAGAREGHLPSVLAMIHVKRCTPIPALLF 371	VADETSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAA 229	LVTFVYVFANIAYVTAMSPQELLASNAVAVTFGEKLLGVMAWIMPISVALSTFGGVNG 333	LTLYLLVFALAARV-LRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVE-ELATWVDRNS 181	FWLEPKNAFENFQEPDIGLVALAFLQGSFAYGGWNFLNYVTEELVDPYKNLPRAIFISIP 275	LSPVRAK 123	161 GLRL-LAAICLLLLTWVNCSSVRWATRVQDIFTAGKLLALALIIIMGVVQICKGEF 215	ALGUGLAAIAAYWALLSUTDIDLRQATPIHWLVLLYWGVDALATG 109	PKSGGDYSYVKDIFGGLAGELRLMIAVLVIYPTNQAVIALTESNYVLQPLFPTC-FPPES 160	PQQWGHSSFLHRLFGSLRAWRASSQLLVWSEALGGFLLAVVYGSAPFVPSS 64

Search completed: January 10, 2002, 23:09:02 Job time: 304 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

January 10, 2002, 23:04:08; Search time 56.67 Seconds (without alignments) 1205.385 Million cell updates/sec

Title: Perfect score: Sequence: Scoring table: US-09-887-038-3
2426
1 MIVWOTLIFAHYQPQQWGHS.....WQPQPSKQLPPEAEHSDEKM 467 BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL\_17:\*

sp\_phage: \* sp\_archea:\*
sp\_bacteria:\* sp\_organelle:\* sp\_mhc:\* sp\_invertebrate:\* sp\_human:∗ sp\_rodent:\*
sp\_virus:\* sp\_mammal:\* sp\_fungi:\* sp\_unclassified:\* sp\_plant:\* sp\_vertebrate:\*

Pred. No. is the score greater the and is derived by is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, rived by analysis of the total score distribution.

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6.1	6.1	6.2	6.2	0.4	0.0	6.7	6.9	6.9	7.0	7.0	7.1	7.3	7.4	8.0	0.4	00	46.7	100.0	Match Length	Query	de
539	395	461	401	360	198	440	597	422	384	391	438	641	478	443	387	438	474	467			
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			-	Q9xc97 klebsiella	006944 synechocyst	Q9aau5 caulobacter	Q9kuw6 vibrio chol				Q9kyg4 streptomyce				••	Q9kthl vibrio chol	P73958 synechocyst	P72547 synechococc	Description		

Qγ 밁

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Ouery Match 100.0%; Score 2426; DB 2; Best Local Similarity 100.0%; Pred. No. 2.2e-123; Matches 467; Conservative 0; Mismatches 0;

Indels Length 467;

Gaps

9

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241 YSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRV 300

61 VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVG 120 61 VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVG

120

45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	2	20
126.5	127	127	127.5	127.5	128	128.5	128.5	129	129.5	130	130	130.5	131	131.5	133.5	133.5	134	134	137.5	137.5	138	138.5	139.5	139.5	144.5
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031199	Q9ryk7	053150	Q9a4e2	Q910u5	Q5152 <b>4</b>	Q9hs12	091726	Q9yq70	068200	Q9ke20	Q916a1	091134	080905	Q9kyw0	P72627	Q9r9w6	Q9i2b6	Q9ks12	Q9ru99	Q9keh4	Q9rrk1	Q9zit8	Q9a5z6	Q9rtz5	Q9zg09
pseudomonas	deinococcus	mycobacter	caulobacter	pseudomonas	pseudomonas	halobacter	pseudomonas						5 arabidopsis							bacillus ha		-			thiobacillu

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Best Local S
Matches 223
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Synechocystis sp. strain PCC6803. II. Sequentize genome and assignment of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M. Tabata S.;
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01-FEB-1997 (TIEMBLIEL 02, La
01-JUN-2001 (TIEMBLIEL 17, La
01-JUN-2001 (TIEMBLIEL 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001457; Oxidored_q3.
Pfam; pF00499; oxidored_q3; 1.
Hypothetical protein; Complete pr
SEQUENCE 474 AA; 52241 MW; 01
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Bacteria; Cyanobacteria; Chroococca
NCBI_TaxID=1148;
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                                                                                 YSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLL--VAVLGLEPL
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RVRVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTAL
                                                                                                                         STLAQATRVYSFLGNPNLLAAYLVPMTGLSLSALVVWRRWWPKLLGATMVIVNLLCLFFT
                                                                                                                                        LAKLTANICLFLLAARLLQNKQWLNRLVTVVLLVGLLVGSYGLRQQVDGVEQLATWNDPT
                                                                                                                                                                                                                              LAKLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRN
                                                                                                                                                                                                                                                                 TSTIMIGIEMLLCGAFWALLIFADQPGKGLTPIHVLVFAYWCISAIAVGFSPVKMAAASG
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SEQUENCE
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STRAIN=EL TOR N16961 /
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AL PROTEIN VC0931.
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24.7%;
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Last sequence up
Last annotation
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8; Mismatches
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Pred. No. 0.00046;
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303 LVHGMVDTVWYRPPVSTLWWLLVAIVASQWASAQARLEASKEENEDKPL LGHGLFDTYLYRPEASTLWWLCIGAIASFWQPQPSKQLPPEAEHSDEKM SAYSIYLEILVETGVVGFTCMLWLLAVTLGKGVELVKRCRQTLAPEGIWIMGALAAIIGL SAYSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGM RLRAMSIFAGREDSSNNFRINVWEGVKAMIRARPIIGIGPGNEAFNQIYPYYMRPRFTAL 467 473 422 362

MEDLINE-20406833 PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M. Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Selle McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter Fraser C.M.; subdivision; Vibrionaceae; update) CRC64; pathogen Vibrio Gwinn M.L., Vibrio. Sellers P.,

SAPFVPSSALG-LGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRA 115 QTLTFAHYQPQQWGHSSFLHRLF-----GSLRAWRASSQLLVWS--EALGGFLLAVVYG DRPWLGIGPGNTAFNLVYPLYQQARFTAL--SAYSVPLEVAVEGGLLGLTAFAWLLLVTA APWRRWLFPVVLGGLVAVLLVAVLGLEPLRVRVLSIFVGREDSSNNFRINVWLAVLQMIQ NTLKKLLAILLSDKAFIRLGLVIMVIALVLTRSRMGNIAFFVALSIGSLLILLFYKSK------LNQWIYGVEELATWVDRNSVADFTSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVWR LVFISAVKSLHYLQICLVAALLVDTPHKLKMLATTMIASGICQAFYAGVILLLELQTSPFAALVGLAKLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYG------PKSLYLLIVSLFIVDALVVSNWFGLDKVRQR-----LAETSLQNESRDDVVRDALNAIQ -LGCLFLLPAAQCWLAIQRAKVIL---IPVALFTLWSWMQSWPSLGLSSDQT -SFVYHNHLANFL-MLNLCLGFGLLIAELNHQTTQ-----GWR -SLCLILTYSRGGWLGFVAMIFVWALLGLYWFQPRLP : |:|| | ::::: -----AWSLNEIYVAFLL----150 197 218 269 42 56 387 309 329 255 162 90

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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
NCBI_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 43.0 KDA PROTEIN.
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LCLYNLFDVTIFDMRNNVLGWIFLAAIAGVSQRYGTK 374
                                                   MLGHGLFDTVLYRPEASTLWWLCIGAIASFWQPQPSK
                                                                                                                                                                                                                                                                                                                                                        S-AAAIGVWRGW-
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                                                                                                      MMLGETGLIGTALMLGAVGFILAQGMVLLI-----HLSRGGGFRRRSQHLLLLSYGIAFAA
                                                                                                                                                                                                                LYPDRYRTALRSTQWQFSWDMFLDQPIFGQGLRNFT----PLYQAAMNVWIGHPHNLVL
                                                                                                                                                                                                                                                                   ---EDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALS-AYSVPL
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                                                                                                                                                            EVAVEGGLLG----LTAFAWLLLYTAVTAVRQVSRLRRD----RNPQAFWLMASLAGLAG
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                                                                                                                                                                                                                                                                                                                         -WLV-ALAGGATAMVLWASFGPFGKEPLRQIVPKYFWGRLSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LPKLL--AIAATGASSLCLILTYSRGGWLGFVAMIFVW
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Pred. No. 0.00
54; Mismatches
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81D6C8DFCA25A1C9 CRC64.
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No. 0.00071
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RA Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Cristofani M., Dias Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.B.,
RA Facincani A.P., Ferreira M.J.S., Ferreira V.C.A., Ferro J.B.,
RA Facincani A.P., Ferreira G.A.G., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambals M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukma A.Y.,
RA Mania A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto J.B.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Silva A.C.R., de Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva F.M., Santelli R.V., Sawasaki H.E.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meddains J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa.";
LENEL: Alpola R.G., La R.G., Santelli R.C., La R.G., Santelli R.C., La R.G., Santelli R.C., La R.G., Santelli R.G., Santelli R.G., Santelli R.G., Santelli R.G., Santelli R.G., Santelli R.G., Sant
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Q9PH43;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR InterPro, IPR003439, ABG_transportr.
DR HOSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
SO SEQUENCE 478 AA; 52495 MW; 6C4F36DABAFF70F1 CRC64;
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Mierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K Nierman W.C., Feidblyum T.V., Laub M.T., Ohta N., Maddock J.R., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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-AQGKRARVVVMIGG--AAVLLAAVGLAMRSADITAARLENLDGDVATRQTIFAAHWQAF
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"A set of ordered cosmids and a detailed
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Pseudomonas putida.
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SEQUENCE 391 AA; 43109 MW; 4658DF8489DB64B
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"Cell envelope mutants of Pseudomonas putida: p
characterization and analysis of their ability
Environ. Microbiol. 1:479-488(1999).
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Q9RZA8;
01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2001 (TrEMBLrel. 16, La
HYPOTHETICAL 41.9 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   radiodurans R1.";
Science 286:1571-1577(1999).
Science 286:2; AAF12372.1;
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hes 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIALV----PVFPP-----LYLAALACLGSLRTLP-----QAAR---GVLFFFAATQLIAA 64
                                                                                                                                                                       PYLTYLEKDGCQLTPTLQRNKIECPQQLSRWSSVWLIAHNAWLHWLLESGIIGLSG----
                                                                                                                                                                                                                                 FNLVY-----PLYQQ
                                                                                                                                                                                                                                                                                           LAAFATTSLNVPFKPLDRLLNDQTSGRE-----YVWQDAVSGWETSPLGGVGPYQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGVEELATWVDRNSVADFTSRV---YSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKL
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                                                         LLAIMVYALWRAIQL---GDP-----FTLAVLYGFTAMNVVDVVIAVPSPHFSELWWVC
                                                                                                             LLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLGHGLFDTVLY--RPEASTLWWLC
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26.7%; Pred. No. 0.
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Last annotation updat
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09A5L8;
01-JUN-2001 ('
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HYPOTHETICAL
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Q9KUW6;
01-OCT-2000
                                                         Q9KUW6
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TIGR; CC2429; -.
Hypothetical protein; Complete proteome.
SEQUENCE 422 AA; 45786 MW; 656279D26E34E1FF CRC64;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=21173698;
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                                                                                                                                                                                                   FYLQTMSLAVVAVYRER
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
L PROTEIN CC2429.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 168; DB 2; Length 422; Pred. No. 0.049;
Created)
                                                         PRT;
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RESULT
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AC Q9
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Best Local S
Matches 109
  Q9AAU5;
Q9AAU5;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-19952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M. Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Cill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Oin H., Dragoi I., Selle McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000215; Serpin.
PROSITE; PS00284; SERPIN; UNKNOWN_1.
Hypothetical protein; Complete prote
SEQUENCE 597 AA; 67451 MW; D3351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:477-483(2000).
EMBL; AE004127; AAF93566.1;
TIGR; VC0393; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
01-JUN-2001
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                                                                                                                   QLEYPFYH---
                                                                                                                                        LFDTVLYRPEASTLWWLCIGAIASFWQPQ
                                                                                                                                                                ELLYWGVEGGLLPVMG---ILLAACFCALRIYAAKRGTR---
                                                                                                                                                                                                               ESPRRETEPQTIDMIIEKPFTGYGYGK--FEAQYLLYTARQHQLNSSYPAGLASMDHPHN
                                                                                                                                                                                                                                        NNFRINVWLAVLQMIQDRFWLGIGPGNTAFNLVYPLYQQARFTALSAYSVPLEV-----
                                                                                                                                                                                                                                                                                      FVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRVRVLSIFVGREDSS
                                                                                                                                                                                                                                                                                                                 LVLS------GYLLARQPEKYDSRWSKIGILYATPLLTAPLLVVLASRTGWLASLLSI
                                                                                                                                                                                                                                                                                                                                               TAFSAAAIGVWRGWL-----
                                                                                                                                                                                                                                                                                                                                                                                          VVVITSLFVSVYGLNQWIYGVEELATWVDRNSVADF---TSRVYSYLGNPNLLAAYLVPT
                                                                                                                                                                                                                                                                                                                                                                                                                      LWLSCALLT--LPITYSNADWFHTLGRLVGLWAGFTLFLVLQQF--RFSNKHKQRLLWF-
                                                                                                                                                                                                                                                                                                                                                                                                                                            YWGVDALATGLSPV------RAAALVGL-AKLTLYLLYFALAARVLRNPRLRSLLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FALAVVYLLAMHFFMPNPGGAGLALSFNTTVWIATSITLAIGLYQLANNQALRYSKLTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLAVVYGSAP--FVPS-SALGLGLAAIAAYWALLSLT-----DIDLRQATPIHWLVLL
                                                                                                                                                                                     ----AVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLGHG
                                                                                                                                                                                                                                                                                                                                                                      -ILLGSVIEAVIGLIQYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
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 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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1 (TrEMBLrel. 17, 1
AL PROTEIN VC0393.
                                                     PRELIMINARY;
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Last
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Pred. No. 0.083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome.
D33513A00836688C CRC64;
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 sequence up
annotation
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             update)
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update)
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Sellers P.,
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RESULT O06944
ID 006
AC 006
DT 011-
DT 011-
DT 011-
DT 01-
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Best Local Similarity
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                                                                                                                                            O06944

PRE-----
O06944; Q55995;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation updat
"VPOTHETICAL 96.7 KDA PROTEIN."
                                                                                                    Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; CRBI_TaxID=1148;
                                SEQUENCE FROM N.A. MEDLINE=96127529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vematheau J., Ermolaeva M., White (Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; Proc. Matl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL; AE005722; AAK22486.1; TIGR; CC0499; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete SEQUENCE 440 AA; 47613 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTSRVYSYLGNPNLLA-AYLVPTTAFSAAAIG-----VWRGWLPKLLAIAATGASSLCL
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  PubMed=8590279;
A., Sato S., Ko
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                                                                                                                                    Chroococcales;
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Pred. No. 0.11;
47; Mismatches 1
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        Kotani
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D90CFCDA3B6C5C5F
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                                                                                                                                 Synechocystis
     Sazuka
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kinura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumu Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiura M., Tabata S.;

Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).
                                                                                          Q9XC97;
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EMBL; D64005; BAA10778.1; -.
HYPOThetical protein; Complete proteome.
SEQUENCE 861 AA; 96682 MW; A064B98C2D9B6C59
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Aguilar A., Tomas J.M.;
"Genetic characterization of the Klebsiella pr
cluster involved in core lipopolysaccharide bi
Submitted (APR-1999) to the EMBL/GenBank/DDBJ
EMBL; AF146532; AAD37765.1; ..
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Search completed: January 10, 2002, 23:10:21 Job time: 373 sec

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Copyright (c) 1993 - 2000 Comp
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4.5	44	3	42	4	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
34.2	•			34.6	34.8	35 5	35	35	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.6	35.6	35.8	35.8	35.8	36.2	36.8	36.8	37.8	39.2	39.6	39.6	44.4
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22	21	22	18	12	18	20	20	18	21	22	21	19	21	22	20	21	22	21	21	19	19	19	21	22	22	12	20	20	21	21	18	18	21
AAH34854	AAZ36714	AAS06335	AAT77137	AAQ13227	AAT80413	AAX53491	AAX05110	AAT61016	AAC55857	AAF30870	AAA13905	AAV23494	AAC55840	AAC90076	AAZ32019	AAC55785	AA128927	AAA78189	AAA13900	AAV23486	AAV62176	AAV62152	AAZ60909	AAT59252	AAI61038	AAQ13408	AAX34136	AAX34135	AAA10595	AAA58471	AAT99219	AAT99220	AAA10594
Human colon cancer	leotide se	DNA encoding human	Single chain antig	PRV glycoprotein g	Tylactone synthase	Human adenosine Al	S. aureofaciens DN	Total DNA sequence	Complete nucleotid	Pseudomonas alcali	Pseudomonas alcali	Pseudomonas Xpc, O	Complete Mitomycin	L13855 cDNA clone.	3	Type I polyketide	Colon tumour relat	cDNA encoding huma	Pseudomonas alcali	Pseudomonas XcpV s	HSV-2 strain SB5 C	HSV-2 strain SB5 C	Murine delta-relat	Human polynucleoti	Human polynucleoti	Pseudorabies virus	Mycobacterium spec	Mycobacterium spec	Gene encoding a su	Nucleotide sequenc	M. tuberculosis IN	M. bovis INH resis	Gene encoding a su

## ALIGNMENTS

AAH52001 RESULT

AAH52001 standard; DNA; 810

BP.

Mycobacterium tuberculosis potential drug target gene SEQ ID 55.

04-SEP-2001 AAH52001;

(first entry)

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12-NOV-1999;
12-NOV-1999;
01-FEB-2000;
Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                        WPI; 2001-329193/34.
P-PSDB; AAG81150.
                                                                      Eisenberg D,
                                                                                                                                                    13-NOV-2000; 2000WO-US31152
                                                                                                                                                                        17-MAY-2001.
                                                                                                                                                                                            WO200135317-A1
                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                   Drug target; growth; organism viability; characterisation; ds.
                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                            99US-0165086.
99US-0165124.
2000US-0179531.
                                                                      Rotstein SH,
                                                                      Marcotte EM;
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nucleoti

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PRR PRRX PRX PRX X PRX X
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AAQ78915
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14-MAY-1993;
31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
(BANE/) BANERJEE
                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growt or viability of an organism. Polynucleotide sequences AAH51947 - AAH57 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention.
                                                                                                                                   12-MAY-1994;
                                                                                                                                                                                  24-NOV-1994
                                                                                                                                                                                                                             W09426312-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium bovis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ78915 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences
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                                       93NZ-0247620.
93US-0062409.
94US-0221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bovis.
                                                                                                                                   94WO-US05344
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/label= ORF1
1256..2065
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Pred.
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No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INH; InhA gene; pS5 gene;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                           vector pVUBLE and transformed into Mycobacterium smegmati
The smallest plasmid obtained which conferred resistance
the target of action for isoniazid, was designated pS5.
sequence of pS5 was determined (AAQ78915), revealing 2 la
reading frames, the InhA gene comprising ORF2.
                                                     CDS
                                                                                CDS
                                                                                                            Mycobacterium
                                                                                                                                                        Mycobacterium bovis
                                                                                                                                                                                                              AAQ75519 standard; DNA; 2232 BP
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Wilson TM
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(DLIS/)
(JACO/)
(WILS/)
(AGRE-)
                                                                                                                                                                            03-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig. 9A-9D; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene target for isonicotinic prods for diagnosis, treatmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-006366/01.
P-PSDB; AAR66291; AA
                                                                                                                                      Isonazid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mycobacterial
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                                                                                                                                                                                                                                                                   tgcggcgcgatcgcaatccccaagccttttggttgatggctagcttggccggtttgg
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DE LISLE G W.
JACOBS W R.
JACOBS T M.
WILSON T M.
AGRESEARCH.
COLLINS D.
UNIV YESHIVA
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                            bovis G4/100
                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infections
                         /note=
                                   /label=
                                                    /label- ORF1
1256..2062
                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    411
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                                                                                                                                                       pS5 operon
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                        "inhA
                                   ORF2
                                                                                                                                                                                                                                                                                                                                                                                                                  696 C;
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                        gene"
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                                                                                                                                                                                                                                                                                                                                                                      Score 47.4; DB 1
Pred. No. 0.0049;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid hydrazide - used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISLE GW,
                                                                                                                                                                                                                                                                                                                                                                                                                  752 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prevention
                                                                                                                                                                                                                                                                                                                                                                                                                  373 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                            revealing 2 large open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and studies involving
                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WR;
                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                       vaccine;
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WO9426765-A

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                                                                                                                                                                                                                                                     1311
                                                                                                                                                                                                                                                                                                                                              pYUB18 and transferred into Mycobacterium smegmatis mc2155. The smallest plasmid obtained which conferred an isoniazid resistance phenotype on M. smegmatis was designated pS5 Sequencing of pS5 revealed 2 open reading frames, ORF2 corresponding to the inhA gene. Mutants of this gene have been moved in the inhA
                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide(s) determining mycobacterial isonlazid - useful in diagnosis, treatment mycobacterial infection, e.g. tuberculosis.
                                                                 INH resistance; InhA gene;
mycolic acid biosynthesis;
                                                                                         M. bovis
                                                                                                                                                                                                    1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AGRE-)
                                 Mycobacterium
                                                 antibiotic
                                                          HNI
                                                                                                          01-APR-1998
                                                                                                                          AAT99224;
                                                                                                                                          AAT99224 standard;
                                                                                                                                                                                                                                                                                                                              Sequence 2232 BP; 411 A; 696 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banerjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1993;
14-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1994;
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                                                       type antibiotic;
                                                                                                                                                                                                                                                            cgttgagcgcctactccgtcccgctggaagtcgcggttgagggcggactactgggcttga
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                                                                                                                                                                                                                           cggccttcgcttggctgctgctggtcacggcggtgacggcggtgcggcaggtgagccgac 1189
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93US-0062409.
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        Location/Qualifiers 494..1237
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                                                                                                                                          DNA;
                                               y gene; isonicotinic acid hydrazide; mycobacteria;
hesis; antibiotic susceptibility; infection thera;
M. tuberculosis complex; isoniazid; tuberculosis,
strain; pS5 operon; ss.
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Pred. No. 0.0049;
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identification; algal; archaeal; bacterial; fungal; parasitical; microorganism; diagnosis; translation elongation factor Tu; toxin; translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1070 cgttgagcgcctactccgtcccgctggaagtcgcggttgagggcggactactgggcttga 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the coding sequence for a mycobacterial InhA protein. The encoded protein is involved in mycolic acid biosynthesis. The nucleic acids are useful in assessing the susceptibility of various strains of the M. tuberculosis complex to isoniazid (INH) type
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                                                                                                             Mycobacterium tuberculosis nucleotide sequence SEQ
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                                                                                                                                                                                                                                                                                                              Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                      detection of any bacterium, fungus or parasite in a sample and for the detection of at least one antimicrobial agent resistance gene or at least one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group which can be detected include Abiotrophia addacens, Bordetella sp.,
                                                                                                           1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 1488-1489; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
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Picard FJ,
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19-MAY-2000; 2000CA-2307010
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                                                                                                                                                                                                                                                                                                                                                                                                       The gene from Mycobacterium tuberculosis encoding InhA (AAR66901), the target of action for isoniazid, was identified, isolated, cloned and sequenced (AAQ75518). Mutant inhA genes have been used for recombinant vaccine development.
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                            AAQ78914;
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14-MAY-1993;
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(first entry)
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93US-0062409.
94US-0221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-US05398
                                                                                                                                                                                                                                                                                                                                                                              566 A; 995 C; 1037
                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                     3,48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EINSTEIN COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D,
                                                        3120
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                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LISLE GW,
                                                        ВP
                                                                                                                                                                                                                                                                                                                      Score 47.4; DB 1 Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs
                                                                                                                                                                                                                                                                                                                                                                              522 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance
                                                                                                                                                                                                                                                                                                         81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevention
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                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                     3120;
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RESULT
AAT99223
ID AAT9
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AC AAT9
AC AAT9
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Best Local Similarity
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1993;
14-MAY-1993;
31-MAR-1994;
                                                                                                  1161
                                                                                                                    1190
                                                                                                                                       1101
                                                                                                                                                                            1041
                                                                                                                                                                                                                                                                                           Genes from Mycobacterium smegmatis, Mycobacterium tuberculosis Mycobacterium bovis that encode inha, the target of action for isoniazid, were identified, isolated and cloned. Sequences of the 3 genes are given in AAQ78913-15, and encoded amino acids isolated. AAR66289-91. Mutant genes have been used in recombinant vaccing the sequences of the sequences of the sequences.
                                                                                                                                                                                                                                                                                                                                                                        Gene target for isonicotinic acid hydrazide - used to prods for diagnosis, treatment, prevention and studies mycobacterial infections
             01-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DLIS/)
(JACO/)
                                AAT99223;
                                                                                                                                                                                                                                                                Sequence 3120 BP;
                                                                                                                                                                                                                                                                                     development.
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig. 8A1-8C2;
                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BANE/)
                                                   AAT99223
                                                                                                                                                                                                                                                                                                                                                                                                                                          Banerjee A
Wilson TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AGRE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WILS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COLL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis
                                                                    8
                                                                                                                                                                        cgtcgatcgcgtttcacatcgcacgggtagcccaggagcagggcgcccagctggtgctca 1100
                                                                                                          tgcggcgcgatcgccaatccccaagccttttggttgatggctagcttggccggttttgg
                                                                                                                                               cggccttcgcttggttgctggtcacggcggtgacggcggtgcggcaggtgagccgac
                                                                                                                                                                                     cgttgagcgcctactccgtcccgctggaagtcgcggttgagggcggactactgggcttga 1129
                                                                                              1995-006366/01.
                                                                                                                                                                                                                  96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLINS D M.
DE LISLE G W.
JACOBS W R.
WILSON T M.
AGRESEARCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COLLINS D.
UNIV YESHIVA EINSTEIN COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BANERJEE A.
                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Collins
4, Collins D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mycobacteria;
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                                                                                                                                                                                                                 Conservative
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93NZ-0247620.
93US-0062409.
94US-0221742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US05344
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                                                                                                                                                                                                                                                                562
                                                  DNA;
                                                                                                                                                                                                                         3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                               A; 1006 C; 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e acid
                                                  3120
                                                                                                                                                                                                                                                                                                                                                   76pp; English.
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                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrazide;
                                                                                                                                                                                                                Score 47.4; DB 1
Pred. No. 0.0056;
0; Mismatches 8
                                                  ₿₽
                                                                                                                                                                                                                                                                                                                                                                                 prevention and studies involving
                                                                                                                                                                                                                                                               G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs
                                                                                                                                                                                                                                                              512 T; 0
                                                                                                                                                                                                                                  DB 16;
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                                                                                                                                                                                                                81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
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                                                                                                                                                                                                                Indels
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AAV20433
ID AAV2
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AC AAV2
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DT 15-J
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DE Mycc
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KW Mycc
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1161

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standard;

DNA;

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1190 tgcggcgcgatcgcaatccccaagccttttggttgatggctagcttggccggtttgg

1217

1041 cgtcgatcgcgtttcacatcgcacgggtagcccaggagcagggggcgcccagctggtgctca

cggccttcgcttggctgctggtcacggcggtgacggcggtgcggcgggtgagccgac 1189

1160

1100

Mycobacterium tuberculosis; InhA gene; enzyme crystal; herbicide;

Mycobacterium tuberculosis InhA gene

15-JUN-1998 AAV20433; AAV20433

(first entry)

1101 1130

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Query Match
Best Local
                                          Matches
                                                                                                                                         antibiotics, as decoys and as antisense oligonucleotides to prevent the expression of polypeptides associated with isoniazid (also referred to isonicotinic acid hydrazide) resistance, and for the expression of the proteins, which may also have use in immunoassays for the detection of INH resistant strains, in the determination of whether an INH type antibiotic may be effective against tuberculosis, and in the treatment individuals for infection with these strains.
                                                                                                                                                                                                                                           This sequence represents the coding sequence for a mycobacterial Inha protein. The encoded protein is involved in mycolic acid biosynthesis. The nucleic acids are useful in assessing the susceptibility of various strains of the M. tuberculosis complex to isoniazid (INH) type
               1070
                                                                                                               Sequence 3120 BP; 566 A; 995 C; 1037 G;
                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding mycobacterial Inha isoniazid susceptibility and resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                       Banerjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INH resistance; InhA gene; isonicotinic acid hydrazide; mycobacteria; mycolic acid biosynthesis; antibiotic susceptibility; infection therapy; INH type antibiotic; M. tuberculosis complex; isoniazid; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M. tuberculosis InhA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic resistant strain;
cgttgagcgcctactccgtccgctggaagtcgcggttgagggcggactactgggcttga 1129
                                                                                                                                                                                                                                                                                                                                                                                           1997-558202/51
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGRESEARCH NEW
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                                                                                                                                                                                                                                                                                                                     Column 37-40;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0241766
93US-0062409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0241766
                                                    3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZEALAND
                                                                                                                                                                                                                                                                                                                     55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       De Lisle GW,
                                        0;
                                        Score 47.4; DB 1
Pred. No. 0.0056;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASTORAL
                                                                                                               522 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacobs
                                                                                                                                                                                                                                                                                                                                                              proteins -
                                                                  18;
                                          81;
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R
                                          Indels
                                                                     Length
                                                                                                                                                                                                                                                                                                                                                              associated
                                                                     3120;
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AAX21816
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Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis. The present invention describes: (1) a crystallised InhA enzyme in the form of a plate having the space group C2 and the unit cell constants a = 101.1 Angstrom , b = 83.4 Angstrom , c = 192.9 Angstrom , beta = 95 deg. and alpha = gamma = 90 deg.; (2) a crystallised InhA enzyme in the form of a parallelpiped having the space group P21 and the unit cell constants a = 69.0 Angstrom , b = 116.0 Angstrom , c = 65.0 Angstrom , b = 116.0 Angstrom , c = 65.0 Angstrom of a parallelpiped having the space group P6222 and the unit cell constants a = 90 deg.; (3) a crystallised InhA enzyme in the form of a hexagon having the space group P6222 and the unit cell constants a = 120 deg. A knowledge of the crystal structure of InhA (which is the target of isonazid in Mycobacterium tuberculosum) will help in
                                                                                                                                                                                                                                                                          1101
                                                                                                                                                                                                                     1161
                                                                                                                                                                                                                                                1190
                                                                                                                                                                                                                                                                                                     1130
                                                                                                                                                                                                                                                                                                                               1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
           Mycobacterium
                                                                M. tuberculosis
                                                                                                                      AAX21816;
                                                                                                                                                AAX21816 standard; DNA; 3120
                                                                                                                                                                                                                                                                                                                                                            1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crystalline forms of InhA enzyme -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blanchard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x-ray crystallography;
                                      InhA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the InhA gene from Mycobacterium tuberculosis. The present invention describes: (1) a crystallised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YESH ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development of bactericides or herbicides capable of inhibiting
                                                                                                                                                                                                                                                                                                                                            ogttgagogoctactccgtccgctggaagtcgcggttgagggcgggcttactgggcttga 1129
                                                                                                                                                                                                                                  tgcggcgcqatcgccaatccccaagccttttggttgatggctagcttggccggtttgg
                                                                                                                                                                                                                                                                                       cggccttcgcttggctgcttggtcacggcggtgacggcggtgcggcggtgcggcaggtgagccgac 1189
                                                                                                                                                                                                                                                                                                                            cgtcgatcgcgtttcacatcgcacgggtagcccaggagcagggcgcccagctggtgctca 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity.
                                                                                                                                                                                                                  ccgggttcgaccggctgcggctgattcagcgcatcaccggctgccggccaaaggccc 1160
                                     enzyme;
                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Column 15-18; 22pp;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YESHIVA EINSTEIN COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP;
           tuberculosis
                                   inhibitor; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis
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                                                                inhA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        566 A; 995 C; 1037 G; 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agents
                                                               gene.
                                                                                                                                                                                                                                                                                                                                                                                                 3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0. 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dimensional structure; crystallised; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to help in
                                   therapy;
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0.0056;
81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         other;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 3120;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local s
Matches 96
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28-APR-1994;
16-JUN-1995;
21-AUG-1996;
                                                                                                                                 InhA enzyme; Mycobacterium tuberculosis strain H37
enoyl reductase activity; mycolic acid production;
                                                                                                                                                                                                                                                                                                                  1190
                                                                                                                                                                                                                                                                                                                                                                                     1041
                                                                                                                                                                                                                                                                                                                                                                                                          1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the Mycobacterium tuberculosis inhA coding sequence. The invention relates to a method for identifying inhibitors InhA enzyme comprises identifying compounds which fit the catalytic active site of the crystallized enzyme. Inhibitors of the activity of t InhA enzyme can be used for treating Mycobacteria tuberculosis infectic
         28-APR-1994;
21-AUG-1996;
                                                                                                                                                                                                                                                                                              1161
                                                                                                                                                                                                                                                                                                                                        1101
                                                                                                                                                                                                                                                                                                                                                               1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3120 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying inhibitors of InhA enzyme that fits the catalytic active site of useful for treating tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sacchettini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5882878-A.
                                           21-AUG-1996;
                                                                 17-NOV-1998
                                                                                       US5837480-A
                                                                                                            Mycobacterium
                                                                                                                                                                                           25-JAN-1999
                                                                                                                                                                                                                 AAV68212;
                                                                                                                                                                                                                                     AAV68212 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 3-8; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YESH ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                               cgttgagcgcctactccgtcccgctggaagtcgcggttgagggcggactactgggcttga 1129
                                                                                                                                                                   gene nucleotide sequence
                                                                                                                                                                                                                                                                                            tgcggcgcgatcgcaatccccaagccttttggttgatggctagcttggccggtttgg
                                                                                                                                                                                                                                                                                                                                                   cggccttcgcttggctgctggtcacggcggtgacggcggtgcggtgcggcaggtgagccgac 1189
                                                                                                                                                                                                                                                                                                                                                                                   cgtcgatcgcgtttcacatcgcacgggtagcccaggagcagggcgcccagctggtgctca 1100
                                                                                                                                                                                                                                                                                                                                        ccgggttcgaccggctgcggctgattcagcgcatcaccggaccggctgccggcaaaggccc
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
96; Conserv
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94US-0234011.
95US-0491146.
96US-0701062.
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96US-0700306
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       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cellulose synthase;
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                                                                                                                        WPI; 2000-342371/30.
P-PSDB; AAY85179.
                                                                                                                                                                                                                                                                                                              26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vigna angularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene encoding a subunit of cellulose
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                                                                                                                                                                                          (MIZU/) MIZUNO K.
(OJIP ) OJI PAPER CO
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                                                                                                     DSTCYTRCRCSRNCYSTYSYSSTYRASTTBTT--YCYTCTBCSRRCYSSRYSSTCNCYSY
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Pred. No. 0.055;
)9; Mismatches 659;
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Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                   M. bovis INH resistance gene
                                                                                                        Banerjee A,
Wilson TM;
                                                                                                                                                                       12-MAY-1994;
14-MAY-1993;
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                                                                                                                                                                                                                                                                 US5686590-A
                                                                                                                                                                                                                                                                                           Mycobacterium
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                        Nucleic acids encoding mycobacterial InhA isoniazid susceptibility and resistance
                                                                  WPI; 1997-558202/51.
P-PSDB; AAW40806.
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93US-0062409.
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                                                                                                                                                                                                                                                                                                                                                 INH resistance; InhA gene; isonicotinic acid hydrazide; mycobacteria; mycoblic acid biosynthesis; antibiotic susceptibility; infection therapy; INH type antibiotic; M. tuberculosis complex; isoniazid; tuberculosis; antibiotic resistant strain; ss.
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                          Claim 1; Column 19-22;
                                                  Nucleic acids encoding mycobacterial InhA isoniazid susceptibility and resistance
                                                                                                                                  Wilson
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14-MAY-1993;
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                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
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                                                                                           P-PSDB;
                                                                                                          NPI:
                                                                                                                                              Banerjee A,
                                                                                                                                                                          (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC
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                                                                                           1997-558202/51.
DB; AAW40805.
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12291..15491
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/note= "ORF 30;
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15488..21013
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/note= "ORF 27;
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/note= "ORF
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/note= "ORF 29;
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29372 caggcggc 29379
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL REFERENCE AUTHORS TITLE RESULT SPU62616 LOCUS ACCESSION VERSION KEYWORDS REFERENCE SOURCE DEFINITION o 0 0 00000 0 0 O O 000 TITLE ORGANISM AUTHORS REATER TO THE TERM OF THE TER U62616 U62616.1 Bacteria; Cyanobacteria; Chroococcales; Synechococcus.

1 (bases 1 to 4957)

Bonfil,D.J., Lieman-Hurwitz,J., Ronen-Tarazi,M. and Ka Genomic region involved in ability of Synechococcus PC grow under low CO2 conditions

Unpublished SPU62616 4957 bp Synechococcus PCC7942 and putative proteins complete cds. 2 (bases 1 to 4957) Bonfil,D.J., Lieman-Hurwitz,J., Direct Submission Synechococcus sp. PCC 7942. Synechococcus sp. PCC 7942 2 1 4957 2 1 4957 2 1 7218 4 810 4 810 4 823 4 1789 4 2232 4 3120 4 3120 4 3120 4 3120 4 3120 4 3120 2 10732 0 20021 0 27488 9 45335 8 1723 9 37457 1 8 16835 1 7 17214 2 7 17214 2 7 17214 2 7 17214 2 7 17214 2 7 11477 2 7 13655 2 7 AC092316 AC022095 SCC57A DMOVO AE007016 AE0070184 AE005006 AC087726 RCAMCPAB AE004561 AE004771 SC6G10A RME603647 173541 173542 173542 AE004772 AP002999 AE004730 AF254803 DNA BCT 18-SEP-1996 putative protein (dc11) gene, partial cds, (dc12), (dc13), (dc14) and (di33) genes, ALIGNMENTS Ronen-Tarazi, M. Z80108 Mycobacteri AE005006 Halobacte AC087726 Chlamydom L48927 Rhodobacte AC027491 Homo sapi AL137166 Streptomy AC004928 Homo sapi AX164174 Sequence AF077869 Streptomy AF210249 Streptomy AF210249 Streptomy AC025336 Homo sapi UT1383 Drosophila X59772 D.melanogas AE007016 Mycobacte AP002999 Mesorhizo
AE004730 Pseudomon
AF254803 Burkholde
AC092316 Homo sapi
AC022095 Homo sapi
AC136519 Streptomy
AL603647 Rhizobium
173541 Sequence 1
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/note-"similar to Synechocystis PCC6803 cyanobase N.
/note-"similar to Synechocystis PCC6803 cyanobase N.
slr1895 and to E. coli and H. influenzae ICC proteins,
Swiss-Prot Accession Numbers P36650 and P44685
respectively; similar to a 12.8 KDa putative protein in
the 16s rRNA gene region of Synechococcus PCC6301,
Swiss-Prot Accession Number P05677"
                                                                                                                                       sequence"
1353. .17
                                                                                                                                                                                                                                                              /translation-"MAMNRAFRFALLSDLHIGLPQTIWHHPHREFLLIECSIPAFEQIL
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WLQQELATSTASQRWYMIHHNVLEHLPDQQOHPLGQRYILENAEELRSILEAGSYSVI
TGTGHLHIQATSQQGALWEVTTGSLVSYPHPYRLGTVQPAAEGWQLELESRRVRSLPDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="encodes a 237. .269
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/note="encodes a putative transmembrane region"
147. .158
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RNILEQQIQTEDEEPJIALQALQSVLRDLSPELQRSLVGQLACNSEGTVLQDGDELING
LLGFDPRTGAVAIGDRIRVGQRLQLHVRDAQTAADDLERQLGQWCRQHATKPAASLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"similar to the C-terminus of a Synechocystis PCC6803 putative protein encoded by GenBank Accession Number D64000 (cyanobase N. s110524)"
                                                                                                                                                                                                                         complement(1311. .1322)
                                                                                                                                                                                                                                                                                                                                                                            /product="putative protein"
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/transl_table=11
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                                                                                                                                                                              /note="encodes
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                                                                  1353. .1748
/gene="dc12"
                                                                                                                                                                                                /gene="di33"
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/strain⇒"PCC 7942"
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3081..3146
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/note="encodes a
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  /note="encodes a putative transmembrane region"
                                             /note="encodes
3102. .3158
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/gene-"dc13"
1998. .2639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"inactivation of this gene produced a high-CO2-requiring mutant; similar to Synechocystis PCC6803 cyanobase N. s1r1515 and to Escherichia coli sodium/pantothenate symporter and a multidrug resistence protein, Swiss-Prot Accession Numbers P16256 and P21441
                                                                                      QPSKQLPPEAEHSDEKM"
                                                                                                              GIGPGNTAFNLVYPLYQQARFTALSAYSVPLEVÄVEGGLLGLTAFÄWLLLVTAVTÄVR
QVSRLRRDRNPQAFWLMASLAGLAGMLGHGLFDTVLYRPEASTLWWLCIGAIASFWQP
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/protein_id="AAB08476.1"
/db_xref="GI:1549376"
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                                                                                                                                                                   FPVVLGGLVAVLLVAVLGLEPLRVRVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWL
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2670. .4073
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/note="encodes a tyrosine kinase phosphorylation site"
2670. _4073
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                                                                     tacggcctcaaccaatggatctacggcgttgaagagctggcgacttgggtggatcgcaac
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/note="encodes a page 1, 4022
/gene="dc14"
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Synechocystis sp. 1
1576593-1719643.
D90911 AB001339 BA
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Synechocystis sp. PCC 6803
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
1 (bases 1 to 143051)
Kaneko,T., Tanaka,A., Sato,S., Kotani,H., Sazuka,T., Miyajima,N.,
Sugiura,M. and Tabata,S.
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome
DNA Res. 2 (4), 153-166 (1995)
2 (bases 1 to 143051)
Kaneko,T., Sato,S., Kot
Miyajima,N., Hirosawa, Miyajima, N., Matsuno,A
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Hirosawa,M., Sugiura,M., Sasamoto,S., Ki
Matsuno,A., Muraki,A., Nakazaki,N., Naru
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          Kimura,T
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Submitted (28-JUN-1996) Satoshi Tabata, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:tabata@kazusa.or.jp, URL:http://www.kazusa.or.jp/cyano/,
Tel:81-438-52-3933(ex.2330), Fax:81-438-52-3934)
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                                                                                                                                               complement (802)
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unknown protein"
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/product="proline-trnA ligase"
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/protein_id="BANB008.1"
/db_xref="GI:1653092"
/translation="MWDNGSVRHLPRLIMRLSQMLFYTLRDDPADAEIPSHKLLVRAG
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//tams1ation="mmksllrgialsysvlmatggyglttsaqvapgddiptvqeald
tpdvdditdgpdplttwilegeggkaemtswmnnlannqnmvcthgqsnpfwe"
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REFERENCE AUTHORS TITLE JOURNAL

1 (bases 1 to 7218)
Dorner, F., Scheiflinger,F. and
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-

Falkner, F

Gunter

Location/Qualifiers

FEATURES

VERSION KEYWORDS SOURCE

166494 Sequence 166494

7218 bp 14 from patent

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5670367

28-DEC-1997

ORGANISM

Unclassified Unknown. Unknown 166494.1

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1 (bases 1 to 810)
Leung, E. T. Y. and Yam, W.C.
New mutant of isoniazid resis
                                                                                 FL
                                                                                                                   2 (bases 1 to 810)
Leung, E.T.Y. and Yam, W.C.
                                                                                                                                         Unpublished
                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                         Mycobacterium tuberculosis
                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                           AF106077.1
                                                                                                                                                                                                                                                                               carrier_protein reductase (inhA) gene, complete
                                                                                          Submitted (12-NOV-1998) Microbiology,
                                                                                                       Direct Submission
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1491 c 1486 g
                       /db_
                                   /organism="Mycobacterium
/strain="IR12269"
                                                                  Location/Qualifiers
/gene="inhA"
                                                                                                                                                                                                                                                           GI:4588369
                       xref="taxon:1773"
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                                                                                                                                                                                                                                         Submitted (11-OCT-1993) Asesh Banerjee, Microbiology a Immunology, Albert Einstein College of Medicine, 1300 Avenue, Bronx, NY 10461, U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                     Banerjee, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                          Banerjee,A., Dubnau,E., Quemard,A., Wilson,T., Collins,D., de Lisle,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein (inhA) gene,
U02492
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                                                                                                                                                                                                                                                                                                                                                                                                                      inhA, a gene encoding a target for
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96; Conservative
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/gene="inhA"
22. .831
/gene="inhA"
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11. .16
22. .831
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EEGWDQRAPIGWNMKDATPVAKTVCALLSDWLPATTGDIIYADGGAHTQLL"
250 c 281 g 136 t
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rligritdrlpakaplleldvqneehlaslagrvteaigagnkldgvvhsigfmpqtg
mginpffdapyadvskgihisaysyasmakallpimnpggsivgmdfdpsrampaynw
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/db_xref="GI:4588370"
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/clone="pyuB 315"
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                                                                                                                                                                /strain="H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U41388
U41388.1
                                                                                                                                                                                   Submitted (27-NOV-1995) D.M. Collins, Animal Health Division, Agresearch, Ward Street, Upper Hutt, P.O. Box 40063, New Zeal
                                                                                                                                                                                                                                                                                                                                  Wilson, T.M., de Lisie, G.W. and Collins, D.M. Effect of inhA and katG on isoniazid resistance and virulence
                                                                                                                                                                                                                                                                                                                                                                                                             inhA, a gene encoding a target for isoniazid and ethionamide in Mycobacterium tuberculosis Science 263 (5144), 227-230 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banerjee, A., Dubnau, E., Quemard, A., Wilson, T., Collins, D., de Lisle, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 1789)

Banerjee, A., Dubnau, E., Quemard, A., Balasubramanian, V., Um, K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                               Collins, D.M.
                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis
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                                                                                                                                                                                                                                                                                 95349387
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256 c 285 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="inhA peptide (AA 1-269)"
/protein_id="AAC43210.1"
/db_xref="GI:407314"
/gene="inhA"
163. .906
                                                   /gene-"inhA"
                                                                                        /strain="WAg201"
/db_xref="taxon:1765"
                                                                                                                             /organism="Mycobacterium
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                                                                                                                                                                 ocation/Qualifiers
                                       . 162
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54.2°;
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                                                                                          infections using an INHA gene Patent: US 5686590-A 12 11-NOV-1997;
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Jacobs, W.R. Jr., Col
                                                                                                                              Methods and compositions
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/protein_id="AAB60183.1"
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                  /organism="unknown"
696 c 751 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MTATATEGAKPPPVSRSVLVTGGNRGIGIAIAQRIAADGHKVAVTHRGSGAPKGLEGVECDVTDSDAVDRAFTAVEBHQGPVEVLVSHAGLSADAFLMEMTE
THRGSGAPKGLEGVECDVTDSDAVDRAFTAVEBHQGPVEVLVSHAGLSADAFLMEMTE
EKFEKVINANLTGAFEKVAQRASRSMQENKFGEMIFIGSVSGSWGIGNQAWAASSAGV
IGMARSIARELSKANVTANVVAPGYIDTDMTRALDERIQQGALQFIPAKRVGTPAEVA
                                                                        Location/Qualifiers
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EEGWDQRAPIGWNMKDATPVAKTVCALLSDWLPATTGDIIYADGGAHTQLL"
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conceptual translation supplied by author
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126125.1 GI:1605995
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        Unclassified 1 (bases 1 t
                                    Unknown
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1 (bases 1 to 2609)

Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
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Sequence 2101 from
AX111368
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
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186995.1 GI:3206777
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Crystalline Inha Enzyme-NADH Complex Patent: US 556778-A 1 17-SEP-1996;
Location/Qualifiers
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173545
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Patent: US 5686590-A 11 11-NOV-1997;
Location/Qualifiers
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-APR-2001) The Institute f
Medical Center Dr, Rockville, MD 20850,
Location/Qualifiers
                                                                                                                                                                                         Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E. Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Kolonay,J.F., Delcher,A., Utterback,T., Weidman,J., Khouri,H.
                                                                                                                                                                                                                                                                                                  \mbox{Gill,J.,} Mikula,A. and Bishai,W. Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                   Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome.
AE007022 AE000516
AE007022.1 GI:13881145
                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                         Fleischmann, R.D., Alland, D., Eisen, J.A.,
                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium; Mycobacterium tuberculosis complex.
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Sacchettini,J., Blanchard,J. and Jacobs,W.R. Jr.
Method and compounds for inhibiting lipid biosyn
                                                                                                                                                                                                                                                                                        laboratory strains
                                                                                                                                                                                                                                                                                                                                                                              Fleischmann, R.D., Alland, D., Eisen, J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis CDC1551,
                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                              100.
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/gene-"|
100. .1:
                                                                         /organism="Mycobacterium
/strain="CDC1551"
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995 c 1037 g
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1. .3120
                                          note="clinical
                                                         /db_xref="taxon:83331"
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                                                                                                                                                                                            Khouri, H.,
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/gene="MT1528"
2194. .3201
/gene="MT1528"
                                                                             /gene="MT1530"
4257 .5000
/gene="MT1530"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3274. .4152)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTLPLIGPMTLSGFAHSWEFLFLFVVAGLVALVILMQLARQRRM LFFANNELLESVAPKRPSRWRHVPAILLVLSLLLFTIAMAGFTHDVRIPRRAVVMLV IDVSQSMRATDVEFSRMVAAQEAAKQFADELTFFQINLGILAYAGTATVLFVSPTMREA TKNALDKLQFADRTATGEAIFTALQAIATVGAVLGGGDTXPBARTVLFSDCKETMPTN PDNPKGAYTAARTAKDQGVPISTISFGTPYGFVEINDQRQPVPVDDETMKKVAQLSGG
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/protein_id="AAK45792.1"
/db_xref="GI:13881147"
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PGESRLYQPGDDVRRMDWAVTARTTHPHVRQMIADRELETWLVVDMSASLDFGTACCE
KRDLAVAAAAAITFLMSGGGNRLGALIANGAAMTRVPARTGROHOHTMLRTIATMPQA
                                                                                                                                                                                                                                                                                           GLQVWEERIEPDEICVIEGMRVTTPERTALDLTSRFPLDPAVAAVDALIQATDLKVAD
VEPLIERYRGRRGMKAARAALDLVDGGAQSPKETWLRLLLIRAGFPRPQTQIAVRNEW
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/gene="MT1529"
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                                                          similarity; putative"
                                                                                                                                                                                                           PADIIRRVGEARAFRA'
4257. .5000
                                                                                                                                                                                                                                                                     GWAEAHLDMGWQDIKVAAEYDGDHHLTSRYHYRKDILRHEKVQHRYGWIVVRVVAEDH
                                                                                                                                                                                                                                                                                                                                                     /translation="MTFVGVTQHTSTMTDFFLGSEALAAGVLTPYELRSRYVALHKDV
YVPQGVELTAQLRAKALWLRSRRRGVLAGYSASAFHGAKWIDADLPAAIIDTNRRRAP
                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAK45794.
/db_xref="GI:13881149"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSYNAATLAELRAVYSSLQQQIGYETIKGDASYGWLRLGALALAAAAALLINRRLF
T″
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/db_xref="GI:13881148"
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TYRMGVTPPQAKQILSTGDLLRLQETAANNFVHHALVDYVVRVVFATRKPEQLGMNDV
KSWVAFGASPRASLGITAAARSLALVRGRDYVIPQDVIEVIPDVLRHRLVLTYDALAD
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QFTPDLVPTDIIGTRIYRQGREEFDTELGPVVANFLLADEINRAPAKVQSALLEVMQE
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/protein_id="AAK45791.1"
/db_xref="Gi:13881146"
/translation="MTSAGGFPAGAGGYQTPGGHSASPANEAPPGGAEGLAAEVHTLE
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/transl_table=11
                        /codon_start=
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1272. .2183
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/note="similar to GP:5458705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
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/product="3-oxoacyl-(acyl-carrier-protein) reductase"

CDS

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gene
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AAGHTGLPWPDVHDAGTVSLLOTLRAAVGRRRLRGTINVVLFVPGDVRGLAAGTQFEH
DALAAGEAVIVANPEDGSAYGLVPEEFSYGDVDEAAQSEPLTPELCALSWMVYSLPG
DALAAGEAVIVANPEGGAYGLVPEEFSYGDVANPRGLVEQLLESSRQHRVPDH
PVLEHYELGDAEYALRSAVRSAAEALSTIGLGSSDVANPRGLVEQLLESSRQHRVPDH
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/gene="MT1533"
complement(6834..7700)
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ATSAWSGYSSCTQYVEDIARARRAAGKDAPELYKLRPYEDHDLEVEMFADAITAAAAT
VRGDARLVFTAHSIPTAADRRCGPNLYSRQVAXATRLVAAAAGYCDFDLAWQSRSGPP
QVPWLEPDVTDQLTGLAGAGINAVIVCPIGFVADHIEVVWDLDHELRLQAEAAGIXA
RASTPNADPRFARLARGLIDELRYGRIPARVSGPDPVPGCLSSINGQPCRPPHCVASV
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5834. .6868
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MGINPFFDAPYADVSKGIHISAYSYASMAKALLFIMNPGGSIVGMDFDPSRAMPAYNW
MTVAKSALESVURFVAREAGKYGVRSNLVAAGFIRTLAMSAIVGGALGEBAGQIQLL
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wpmaalgavfilvsvillujvrpavrrritgtggvglgiealegkkavvlgrvardgg
QvkldggvwtarplindgdvfepgdsvtvvQidgatavvfkdv"
8214. .9359
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thrgsgaprglegvecdytdsdaydrafraveehgpfvecutysdaydashamte
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igmarsiarelskanvtanvvapgyidtdwtralderiqqgalqfipakrvgtpaeva
/gene="MT1533.2"
8214. .9359
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/protein_id="AAK45797.1"
/db_xref="G1:13881152"
/translation-"MQFDAVLLLSFGGPEGPEQVRPFLENVTRGRGVPAERLDAVAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity; putative"
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/protein_id="AAK45796.1"
/db_xref="GI:13881151"
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5019. .5828
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                                                                                                                                                                            /product="conserved hypothetical protein"
/protein_id="AAK45799.1"
/db_xref="GI:13881154"
                                                                                                                                                                                                                                                                                                                                                                                             /gene="MT1533.1"
7758. .8192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVTAILHSAWPD"
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/note="identified by Glimmer2; putative"
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/note="similar to
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/note="similar to
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where similarity; putative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Nycobacterium; Nycobacterium tuberculosis complex.

| (bases 1 to 38300)
| (bases 1 to 38300)
| (cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
| (cole, S.T., Brosch, R., Parkhill, J., Gas, S., Barry III, C.E.,
| Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
| Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
| Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S.,
| Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S.,
| Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
| Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
| Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
| Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
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279701 AL123456
279701.1 GI:3261635
                                                                                         Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:1524225.
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Parkhill, J.
available on the World Wide Web. (URL, http://www.sanger.ac.uk/Pi
                                                                                                                                                                                                                                                                                                                                             Nature. 393 (6685), 537-5
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                                              Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                              Deciphering the biology of Mycobacterium
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AVYEISHYIVGVBQLTTTTLRNVVGGMTLEQTLTSTDQINAQNAGLAKAGRPTPEMLAY
RYELRSIDPPPSIQASMEKQMKADREKRAMILTAEGTREAAIKQAEGKQAQILAAE
RRVELRSIDPPPSIQASMEKQMKADREKRAMILTAEGTREAAIKAGRPTPEMLAY
QYLQTLPEMARGDANKYWVYPSDFNAALQGFTRLLGKFGEDGVERFEPSPVEDQPKHA
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.ac.uk/Projects/M_tuberculosis/) CDS have
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DEICVIEGMRVTTPERTALDLTSRFPLDAVAAVDALLQATDLKVADVEPLLERYRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(55...1074)

'gene"Rv1482c," (MTCY277.03c), len: 339. Highly similar /notem"Rv1482c," (MTCY277.03c), len: 339. Highly similar /notem"Rv1482c, (MTCY277.03c), len: 339. Highly similar toM. avium protein TR:007396 (EMBL:AF002133) MAV346. (346 aa), fasta scores; E(): 0, 65.2% identity in 342 aa overlap, slight similarity to GRPE_ECOLI P09372 heat shock protein grpe (heat shock p 197 aa), fasta scores, opt: 139, E(): 0.012, (28.3% identity in 159 aa overlap). Also similar to Rv3517(MTV023.24), 59.0% identity in 273 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Rv1483, (MTCY277.04), fabG1, len: 247. fabG1, probable 3-oxoacyl-[acyl-carrier protein] reductase, identical to M. bovis G1155269 putative ketoacyl acp reductase (247 aa), strong similarity to FABG_ECOLI P25716 3-oxoacyl-carrier protein] reductase (244 aa), fasta scores, opt: 664.E(): 6.8e-35, (44.4% identity in 241 aa overlap; contains PS00061Short-chainalcohol dehydrogenase family signature"
                                                                                            /db_xref="Swiss-prot:048930"
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ekfervinaautgafrvaqrasrsmgrnkfghnifigsvsgsmgignqanyaaskagv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1024. .1029
/note="putative RBS, GATAGG, for Rv1483"
1038. .1781
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/gene="RV1482c"
complement(55..1074)
                                    GVVSFLASEDASYISGAVIPVDGGMGMGH"
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/gene="fabG1"
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/clone="Y277"
                                                                  IGMARS IARELSKANVTANVVAPGY IDTDMTRALDER TQQGALQF I PAKRVGTPAEVA
                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                          transl_table=11/
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/strain="H37Rv"
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/db_xref="GI-524231"
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1800. .2
                                                       /note="Rv1487, (MTCY277.08), len: 144. Highly similar
M. avium TR:007404 (EMBL:AF002133) MAV145. (145 aa),
fasta scores; opt: 667 z-score: 1148.3 E(): 0, 72.5%
                                                                                                                                                                                                                                                                                                                                                                           /gene="Rv1487"
4539. .4973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLLESSRQHRVPDHAPSRALRVLENAAHVDAIIAVSAGLSRLPIGTQSLSDAQRATDA
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/gene="Rv1486c"
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/gene="hemz"
/gene="hemz"
/note-"Rv1485, (MTCY277.06), hemz, len: 344.
/note-"Rv1485, (MTCY277.06), hemz, len: 344.
/ence-"Rv1485, len:
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2615. .3649
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| RLIQRITDLLEAKAPLLELDVQNEEHLASLAGRVTEALIGAGNKLOVMISIGFMEQTG
| MGINPFFDAPYADVSKGIHISAYSYASMAKALLPIMNPGGSIYGMDFDDFRAMPAYNW
| MTVAKSALESVNRFVAREAGKYGVRSNLVAAGPIRTLAMSAIVGGALGEEAGAQIQLL
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/db_xref="SWISS-PROT:P46533"
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/gene-"inba"
/note="Rv1484, (MTCY277.05), inba, len: 269. Identical
toINHA_MYCTU P46533_enoyl-[acy1-carrier-protein] reductase
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       signature"
1790. .179
                                                                                                                                                                                                                                                                                            /gene="Rv1487"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {	t RASTPNADPRFARLARGLIDELRYGRIPARVSGPDPVPGCLSSINGQPCRPPHCVASV}
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dentity in142 aa overlap"
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                                                                                                                                             /gene="fabG1"
/note="PS00061 Short-chain alcohol dehydrogenase family
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RESULT 1
E32986/c
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   BASE COUNT
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/9ene="Rv1488"
/note="Rv1488, (MTCY277.09), len: 381. Similar to
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YBBK_ECOLI (BAND 7/MEC-2 FAMILY) SPREMBE:P77367
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/translation-"mpvaliwliaalvlvgaealtgdmfllmlgggalaasvsswlla
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wpwwAdgavfllvsvlllvlvrpavrrrltqtkgvqlgiealegkkavvlgrvardgg
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/protein_id="CAB02037.1"
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/organism="Vigna angularis"
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                                                   caagatcggccttggctgggcatcggccccggcaataccgcctttaacctggtttatccc
                                                                                  SDYDATBSDNSTNCCYDASRTBTBSTNCYARCYTBYDARCSRDSTYSSRGYDANSTSRYS
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## ALIGNMENTS

RESULT CNS0091P

DEFINITION **LOCUS** 

Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fruit fly. AL053013.1 GI:4934461 AL05301 CNS0091P genomic survey sequence. 925 bp 03-JUN-1999

Insecta;

REFERENCE AUTHORS TITLE Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Muscomorpha; Ephydro 1 (bases 1 to 925)

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

JOURNAL Genoscope.
Direct Submission

COMMENT

Submitted (02-JUN-1999) Genoscope · Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be formal at http://www.macmad.htm. found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.

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KEYWORDS
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/organism="Drosophila m
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/clone_11b="DrosBAC"
/clone="TaxCN37L08"
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HVSMEh0100N13f Hordeum vulgare 5-45 DAP spike
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA
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                                                     Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                         Direct Submission
Submitted (23-UUI-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of I
BACN08C07 of DrosBAC library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 645)
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Seq primer: AATTAACCCTCACTAAAGGG
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                                          pBeloBAC11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Hordeum vulgare 5-45 DAP spike HVcDNa0009 (5 to 45 DAP)"
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
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/db_xref="taxon:4513"
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project

                                                Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                             GSS.
                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                  Direct
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                                                                                  Submission
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/clone="BACN08C07"
/note="end : T7"
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/plasmid-"pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DAA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     gattcaagatcggccttggctg
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BJ__Ba000
                                                                                        Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A. A marker-dense, sequence-ready map of the Bradyrhizobium
                                                                                                                                                                                                                 genomic,
                                                      Bradyrhizobium group; Bradyrhizobium.
1 (bases 1 to 604)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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18.8%;
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                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
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Class: BAC ends
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/lab_host="E. coli"
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A more detailed description of the library
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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MF project grant. The DNA was prepared from embryos by Alain Buch
                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_ib="RPCI-98"
/clone-"BACR19D16"
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC

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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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                                                                             Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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ound through the I.M.A.G.E. Consortium/LLNL at:
             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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                                                                                                                                                                        Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk-. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/note="end : T7"
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                                /clone_lib="DrosBAC"
/clone="BACN04N13"
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/db_xref="taxon:9606"
/clone="IMAGE:3463577"
/clone_lib="NIH_MGC_12"
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Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end prosophila Genome Project (EDGP) - collaboration with the European Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Direct Submission
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACN15E19"
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a 278 c 217 g
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/plasmid-"pBeloBAC11"
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Best Local Similarity 48.5%;
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Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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BG167536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1868)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_89"
/tissue_type="hypernephroma, cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/noticity Vector: pCMV-SPORT6; Site_1: NotI;
/noticity Vector: pC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4452947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Homo sapiens cDNA clone IMAGE:4452947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcggtggctggctgggttttgtcgccatgatttttgtctgggcgttattaggggctctact 787
                                                                                                         tttaacctggtttatcccctctatcaacaggcgcgctttacggcgttgagcgcctactcc 1086
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Plasmid Drosophila melanogaster

Plasmid Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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/clone="BACN16D22"
/note="end : SP6"
a 229 c 106 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Pred. No. 6.1;
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segref@genoscope.cns.fr
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/backfiles1.seq: *
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US-08-241-766-1
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US-08-125-468-1
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US-09-232-191-24
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Sequence 1, Appli
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Sequence 29, Appli
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US-08-232-463-14
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Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                    FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)886-9300
TELEPHONE: (703)883-4109
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: UI
APPLICATION NUMBER: UI
FILING DATE:
APPLICATION NUMBER: EI
APPLICATION NUMBER: EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
                                      IMMEDIATE SOURCE:
                                                                                                                                                                 TELEFAX: (/-
TELEFAX: 899149
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CITY: Alexandria
STATE: VA
                                                              TOPOLOGY:
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                                                                                 STRANDEDNESS:
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US-08-457-862A-6
US-08-457-662A-6
US-08-457-662A-6
US-08-457-332A-4
US-08-457-332A-4
US-08-457-332A-6
US-08-762-214-6
US-08-762-233A-1
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APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: deLISLE, G. W.
APPLICANT: WILSON, T. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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           ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ADDRESSEE: MORRISON & FOERSTER
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CITY: F
STATE:
                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                            ADDRESSEE: MOKKLOU. CURRET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 gcctgcgagcttggcgggcctccagccagctgttggtttggtctgaggcactgggtggct 145
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TELEFAX:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08491146 Patent No. 5556778
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Sacche
                                           TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
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             SEQUENCE CHARACTERISTICS:
LENGTH: 3120
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                          SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sacchettini et al TITLE OF INVENTION: InhA CRYSTALS AND THREE TITLE OF INVENTION: DIMENSIONAL STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1431
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                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS SOFTWARF: PARTY MS-DOS
                                                                                                                              NAME: George, Kenneth P
REGISTRATION NUMBER: 30,259
REFERENCE/DOCKET NUMBER: 96
                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                              ZIP:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                             USA
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54.2%;
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                                                                                                                                                                                              US-08-241-766-11
                                                                                                                                                               Sequence 11, Applia Patent No. 5686590
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                  GENERAL INFORMATION:
                          APPLICANT: COLLING, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: GELISLE, G. W.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: AMETHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AMO TREATING MYCOBACTERIAL INFECTIONS UNMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                      1190 tgcggcgcgatcgcaatccccaagccttttggttgatggctagctttggccggttttgg 1246
                                                                                                                                                                                                                                                                                                                                   1130 cggccttcgcttggctgctggtcacggcggtgacggcggtgcggcgaggtgagccgac 1189
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE:
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OTHER INFORMATION:
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                 JACOBS, W. R.
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MORRISON & FOERSTER
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Pred. No. 0.00062;
0; Mismatches 81;
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                                          MYCOBACTERIAL INFECTIONS USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3120;
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Best Local Similarity
              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb stor
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,011
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Sacche
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
ATTING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1101
                                                                                                                                                                                                                                                                             APPLICANT: Sacchettini et al TITLE OF INVENTION: METHOD AN TITLE OF INVENTION: LIPID BIG
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ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: /JC
CITY: Palo Alto
CTATE: CA
TISA
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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TELEFAX: 706141
                                                                                                                                                                                   ADDRESSEE: Amster, KOLI
STREET: 90 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 494-0792
                                                                                                                                           COUNTRY: USA
ZIP: 10016
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                            STATE: New York
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No. 5702935 yet assigned
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                                                                                                     inch 1.44 Mb storage diskette
                                                                                                                                                                                                                                                                                                METHOD AND COMPOUNDS FOR INHIBITING LIPID BIOSYNTHESIS OF BACTERIA AND
                  US/08/234,011
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Pred. No. 0.00062;
0; Mismatches 81;
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Best Local
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                  1101
                                                                                                                                                     1041 CGTCGATCGCGTTTCACATCGCACGGGTAGCCCAGGAGCAGGGGGGCGCCCAGCTGGTGCTCA 1100
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                                                     1190 tgcggcgcgatcgcaatccccaagccttttggttgatggctagctttggccggttttgg 1246
                                           1161
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ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 96700/271
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: No
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NAME: Pasqualini, Patricia A.
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                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                   FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID
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                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            PAGES:
                                                                                                                                                                                                                                                                                                                                                                                          VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                      cggccttcgcttgctgctgctggtcacggcggtgacggcggtgcggtgaggtgagccgac 1189
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                                                                                                                                                                                                              Score 47.4; DB 1;
Pred. No. 0.00062;
0; Mismatches 81;
                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                          Length 3120;
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US-08-701-062A-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                 OTHER INFORMATION: PUBLICATION INFORMAT
                                                                                                                                                                                                                                                 IMMEDIATE SOURCE: M
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE: inhA oper
ORGANISM: M tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
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PRIOR APPLICATION DATA: no ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 90 Park
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE:
                               PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch 1.44 mb storage diskette COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS-DOS
                                                                                    TITLE:
                                                                                                                                                                                                                   UNITS:
                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE:
DOCUMENT NUMBER:
                  DATE:
                                                   VOLUME:
                                                                 JOURNAL:
                                                                                                  AUTHORS:
                                                                                                                                                  IDENTIFICATION METHOD:
                                                                                                                                                                                                                                      MAP POSITION:
                                                                                                                                                                                                                                                                                                        ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                         HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,259
REFERENCE/DOCKET NUMBER: 96700/296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08701062A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 Park Avenue
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                                                                                                                 INFORMATION:
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FILING DATE:

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Best Local S
                                       Matches
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                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:

NAME: MONROY, GLADYS H.

REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANERJEE, A.
APPLICANT: GELISE, G. W.
APPLICANT: WILSON, T. M.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inha AGENT
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1161 CGCTGCTCGAACTCGACGTGCAAAACGAGGAGCACCTGGCCAGCTTGGCCGGGCCGGG 1217
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1070 cgttgagcgcctactccgtcccgctggaagtcgcggttgagggcggactactgggcttga 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 96; Conserv
                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcggcgcgatcgcaatccccaagccttttggttgatggctagcttggccggtttgg 1246
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                                  Conservative
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                                                    2.8%;
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Pred. No. 0.00062;
0; Mismatches 81
                                                  Score 39.6; DB Pred. No. 0.08;
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                                     Mismatches
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                                                              DB 1;
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                                                                    Length 1723;
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US-08-241-766-2
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                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
                                                                                                                                                                                                                     Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JACOBS, W. R.
APPLICANT: COLLINS, D. M.
APPLICANT: BANKENJEE, A.
APPLICANT: deliste, G. W.
APPLICANT: WILSON, T. M.
APPLICANT: WILSON, T. M.
APPLICANT: WILSON, T. M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN inha AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1028
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                                                                                        1130 cggccttcgcttggctgctgctg-gtcacggcggttgacggcggtgcggcaggtgagccga 1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              968
                                                                                                                                              968 CGTCGATCGCGTTTCACATCGCACGGGTAGCCCAGGAGCAGGGCGCCCAGCTGGTGCTCA 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 12-MAY-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        TYPE:
               ctgcggcgcgatcgcaatccccaagccttttggttgatggctagcttggccggtttgg 1246
                                                                       ctgcggcgcgatcgcaatccccaagccttttggttgatggctagcttggccggtttgg 1246
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                                                                                                                                                                                                                     Similarity 55.1
98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                       2.8%;
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                                                                                                                                                                                                                   Score 39.6; DB Pred. No. 0.08; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1
                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                       79;
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; LOCATION: (181)..(1188)
US-09-334-601-12
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08911853 Patent No. 6048710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                        OPERATION SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1199 atc 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1139 cttggctgctgctggtcacggcggtgacggcggtgcggcaggtgagccgactgcggcgg 1198
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                PRIOR
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                            WUMBER OF SEQUENCES:
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Local Sin
91;
                                                                                                                COMPUTER:
                                                                                                                                                                                                                           STREET:
APPLICATION DATA:
                                                                                                                                                               ZIP: 94304-1013
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                              CITY:
                                 FILING DATE:
                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCACGTTGAGCAGGTCATGGCGGTTGCGGAGGATCCTCTGGATGCTGGAATGCGCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTTGCCGTCCCGCCGCATGTAGCTGCTGGGGCCCCAGAAGATGAACACGGTGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 2.5%;
Similarity 49.7%;
91; Conservative
                                                                                                                                                                                                            Palo Alto
                                                                                                                                                                                               CA
                                                                                                                                                                                                                             925 Page Mill Road
                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                          Gerritse, Gijsbert
                                                                                                           IBM Compatible
                                                                                                                                                                                                                                            Genencor International
                                                                                                                                                                                                                                                                                           EXPRESSION LEVELS
                                                                                                                                                                                                                                                                                                        EXPRESSION
08/699,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35.8;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                          SYSTEM FOR ALTERED
                                                                              2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.5%;
Best Local Similarity 58.7%;
                                                         TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
                                                                                                     REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gerritse, Gijsbert APPLICANT: Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 CGAAGACCATGCCCTGGTGACCCTGAGTGGCTTCGTCGGGGTCG
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               STRANDEDNESS:
                             TYPE:
                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                          LENGTH:
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGCTGCGTGTCACCGTACGGGTGGCGCCTGCGGCCGGAGCGCGGGCTGCAGGGCAAGAT 338
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                                                                                                                                                                                                                                                                                                                                                              94304-1013
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                             nucleic acid
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                                                                                                                                                                  Glaister,
                                                                                                                                                                                                                                                                                                                                                                                       CA
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                                          390 base pairs
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                                                                                        650-845-6504
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linear
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                                                                                                                                                                                                                                                                                                                                 Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM FOR ALTERED LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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Query Match
Best Local Similarity

2.5%; 58.7%;

Score 35.2; DB 4; Pred. No. 0.74;

Length 390;

Matches

61;

Conservative

0;

Mismatches

43;

Gaps

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                                   Query Match
Best Local Similarity
Watches 67; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1090 ccgctggaagtcgcggttgagggcggactactgggcttgacggccttcgcttggctgctg 1149
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38,241
REFERENCE,DOCKET NUMBER: PF,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: CH 00 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESS: No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1203 caatccccaagccttttggttgatggctagcttggccggtttgg 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 24-DEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U:
ZIP: 27709
                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gctgctgctggtcacggcggtgacggcggtgcggcaggttgagccgactgcggcggatcg 1202
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Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO. V
                                                                                                                                                                                                                                             710 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08998416
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Philippsen, Peter
                                                                                                                                                   PAG1464UP
                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                             919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6239264th Carolina
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                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                             single
                                                                 2.5%;
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                                                  0;
                                                               Score 35.2; DB Pred. No. 0.97;
                                                   Mismatches
                                                                              DB 4;
                                                  53;
                                                                              Length 710;
                                                  Indels
                                                0;
                                                Gaps
                                                0;
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Sequence 29, Application US/0947940
Patent No. 625106
GENERAL INFORMATION:
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
                                                                                                                        US-09-479-409-29
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                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                              14081 GATGCTGCGTGTCACCGTACGGGTGGCGCTGCGGCCGGAGCGCGGGCTGCAGGGCAAGAT 14140
                                                                                                                                                                                             14141 CGAAGACCATGCCCTGGTGACCCTGAGTGGCTTCGTCGGGGTCG 14184
                                                                                                                                                                                                                                                                                1143 gctgctggttgacgggggtgacggcggtgaggtgaggcgactgcggcggcgggtgatcg 1202
                                                                                                                                                                                                             1203 caatccccaagccttttggttgatggctagcttggccggtttgg 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/69 FILING DATE: 16-AUG-1996 ATTORNEY/AGENT INFORMATION: NAME: Glaister, Debra J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gerritse, Gijsbert APPLICANT: Quax, Wilhelmus J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 CGGGTCCTCGCGGCGCCTTGGCCGGCGGGTCCACGGCACGCCGCGGACCTTGAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Geneauca ADDRESSEE: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304-1013
                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                      Application US/09479409
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                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                   2.5%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 35.2;
                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                   Length 17612;
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EXPRESSION SYSTEM FOR ALTERED EXPRESSION LEVELS

NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:

STREET: ADDRESSEE:

3: Genencor International 925 Page Mill Road

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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-125-468-1
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08125468 Patent No. 5589385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.5%;
Best Local Similarity 58.7%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14141 CGAAGACCATGCCCTGGTGACCCTGAGTGGCTTCGTCGGGGGTCG 14184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14081 GATGCTGCGTGTCACCGTACGGGTGGCGCCTGCGGGCCGGGGCTGCAGGGCAAGAT 14140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: lin-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1203 caatccccaagccttttggttgatggctagctttggccggttttgg 1246
                                                                                                                                                                                                                                                  APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fantini, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlortetracycline and tetracyline Formation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                STREET:
                                                                                               ZIP: 07470
                                                                                                            COUNTRY:
                                                                                                                                                 CITY: Wayne
                                                                                                                                                                                   ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/479,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'RY: USA
94304-1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
                                                                                                                              New Jersey
                                                                                                                                                                One Cyanamid Plaza
                                                                                                                USA
                                                                                                                                                                                                                                         useful therein
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Pred. No. 4.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC361-2
     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 17612;
       #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                            ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (gen
US-08-125-468-1
                                                                                                                                                          Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 30001 base pairs
TYPE: nucleic acid
                                                    27865
                                                                                                         27805
 27925
                                                 1057 gegegetittaeggegttgaagegeetaetteegteeegetggaaagteggeggttgaaggegga 1116
                         1177
                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (201)831-3241
TELEFAX: (201)831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               NAME: Tsevdos, Estelle J
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 22-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
 CTGGTCGGCGTCGTCCGCC
                     caggtgagccgactgcggc 1195
                                                                                                       74;
                                                                                                                                                                    h 2.5%;
Similarity 53.2%;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/125,468
27943
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                                                                                                                                                             0;
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                                                                                                                                                                       Score 35; I
Pred. No. 5.
                                                                                                                                                             Mismatches
                                                                                                                                                                         DB 1;
5.9;
                                                                                                                                                             65;
                                                                                                                                                                                    Length 30001;
                                                                                                                                                             Indels
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Gaps

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Search completed: January 10, Job time: 2861 sec 2002, 22:26:54

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